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Minimum DB seq
Maximum DB seq
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Perfect score:
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length: 2000000000
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Listing first 45 s
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em_htgo_rod:*
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em_htg_rod:*
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Compugen Ltd.
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2041.046 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Score Match Length DB ID Description	ſ	,	n ·	ი			c	ဂ			a	C	ი		C		O	ი		C		o							O	G		O		C	ი .	ი				a					a	Result
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ALIGNMENTS

RESULT 1
AC092873/c
LOCUS
AC092873/c
LOCUS
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AC092873 171413 bp DNA
DEFINITION
Pan troglodytes clone RP43-22I12, WORKING DRAFT SEQUENCE, 5
ACCESSION
AC092873
VERSION
AC092873 GI:15055306
KEYWORDS
VERSION
AC092873.1 GI:15055306
KEYWORDS
Chimpanzee
Pan troglodytes
Cource
Chimpanzee
Pan troglodytes
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 171413)
Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L.,
Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E.,
Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, Y.B.,
Masiello, C., Mastrian, S.D., McCloskey, J. C., McDowell, J.,
Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S.,
Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L.,

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COMMENT
                                                                                         BASE COUNT
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walker,M:A., Wetherby,K.D., Zhang,L.-H. and Green,E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                         53796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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Quality coverage: 15.61x in Q20 bases; agarose-fp
Quality coverage: 14.12x in Q20 bases; pulse-field-gel
Quality coverage: 13.87x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 170160 bases at least Q40 Consensus quality: 170445 bases at least Q30 Consensus quality: 170654 bases at least Q20 Insert size: 152000; agarose-fp Insert size: 168000; pulse-field-gel Insert size: 171013; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of Chemistry: Dye-terminator Big Dye; 100% occupansembly program: Phrap; version 0.990319
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Center clone name: 022I12
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/note="assembly_fragment"
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/clone="RP43-22I12"
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Pred. No. 1.8;
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KEYWORDS
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On Feb 11, 2001 this sequence
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Website:http://hgc.igtp.ac.cn
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                                                                                                                                                                                                                                                                                                                              Contact:hgc@igtp.ac.cn
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---- Summary Statistics vector: pUC18; 100% of reads Dye-terminator: ET 55% of reads
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On Feb 3, 2000 this sequence version replaced gi:6684192.

* NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                            TITLE
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Unpublished

2 (bases 1 to 166156)

Li.G., Hu.S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W.,

Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X.,

Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Wang,X.,
                                                                                        1 (bases 1 to 166156)
Xlong,H., Zhou,Y., Dong,H., Lin,W., Chen,B., Zhang,C., Zhang,Y.,
Cai,Z., Ying,H.F., Wang,H., Gu,W., Zhu,G., Tu,Y., Zhang,X., Jia,J.,
Shen,H., Zhang,D., Wu,C., Lu,G., Zhong,M., Jiang,H., Ren,S., Fu,G.,
Chen,Z. and Huang,M.
                                                                                                                                                                                                                                                                                  Homo sapiens chromosome
                                                                          Chromosome 3p genomic sequence
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           Homo sapiens
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/clone="RP11-322F9"
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contig of 9716
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contig of 24647 bp in
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gap of unknown length
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107 gttttcgcagaaacatgc 124
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                                                                                                                              TGAAAAGACTATTTTGTACACCTTTGTGCAAATATATTTGAAAATCTAGAAGTGAAATACAA 108960
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Website:http://hgc.igtp.ac.
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Yang, H.
Direct Submission
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On Mar 6, 2001 this sequence version
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F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                         27;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 166156;
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                                                                                                                                                                                                                                                                                                         0;
         RESULT ACORPORES ID ACORPORES I
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Ying H.F.,
Zhang D., W
Huang M.;
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Db 108961 TATTTCTTAGAAAAATAC 108978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou Y., Xiong H., Dong H., Lin W., Chen B., Zhang (Ying H.F., Wang H., Gu W., Zhu G., Tu Y., Zhang X., Zhang D., Wu C., Lu G., Zhong M., Jiang H., Ren S., Huang M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record was originally submitted Center at Shanghai (CHGC), and now mentains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center:Beijing Center Center code:Beijing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //www.chgc.sh.cn http://hgc.igtp.ac.cn
//www.chgc.sh.cn http://hgc.igtp.
nomics.org.cn Contact:hgc@igtp.
cord was originally submitted by Chinese
cord was originally submitted by CHGC,
                /rpt_family="LTR/Retroviral"
/rpt_unit=MLT2FB
2167...2705
                                                                                                                                                                                                                                                           1030.
                                                                                                                                                                                                                                                                       /clone="RP11-204c23"
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/clone="RP11-8203"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                    /rpt_family="LINE/L1"
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Last upd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of
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a J., Shen
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rpt_unit=MIR

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2709. .3765

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complement(20835. .21083)
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                                               complement(20515. .20823)
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/rpt_unit=(CA)n
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                                                                                                                                                          Conservative
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30901...31101
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/rpt_mit=Ar_rich

/rpt_unit=Ar_rich

27907 .28148
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21753. .22022
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'rpt_unit=AT_rich
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'rpt_unit=THE1B
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/rpt_unit=AT_rich
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/rpt_unit=AluJo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Direct Submission

Submitted (28-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 25, 2000 this sequence version replaced gi:9255957.

Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Parter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
Oswal, G., Parish, B., Paxton, S., Samuel, S., Say, J., Scherer, S.,
Oswal, G., Parish, B., Paxton, S., Samuel, S., Say, J., Scherer, S.,
Shah, E., Simon, M., Sparks, A., Stamps, A., Sucgang, R.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M.,
Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,
Weinstock, G., Weinstock, I.R., Williamson, A.,
Rock, M., Weinstock, G., Weinstock, I.R., Williamson, A.,
Rock, G., Weinstock, G., Weinstock, I.R., Williamson, A.,
Rock, M., Weinstock, G., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 181870)

Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished 2 (bases 1 to 181870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K., Bodocta,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burkett,C., Burrows,J., Carter,M., Chacke,J., Chen,Z., Cox,C., Burkett,C., Deshazo,D., Ding,Y., Domah-Rashid,N., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K., Wren, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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AC024216 AC006431
AC024216.16 GI:9438304
AC024216.16 GI:9438304
                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                               as soon as i
be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 156457 bases at least 040
Consensus quality: 176318 bases at least 030
Consensus quality: 176318 bases at least 020
Estimated insert size: 168203; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: HAGO Center clone name: RP11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web
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29896: contig of 29896 bp in
29996: gap of unknown length
44416: contig of 14420 bp in
44516: gap of unknown length
63362: contig of 18846 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project Information
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                                                          /clone="RP11-204C23"
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                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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1: contig of 1134
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f unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-DEC-1999) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, 100101, P.R.China On Feb 3, 2000 this sequence.version replaced q1:6684200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bao,Q., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Q1,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Wang,X., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 188432)

Wu Q., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H.,
Liu,B., Bao,W., Sun,Y., Wang,X., Wang,H., Yang,X., Cheng,C.,
Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B.,
Fan,H., Liu,Y., Li,G., Li,C., Bao,J., Wang,X., Song,L.,
Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M.,
Chromosome 3p genomic sequence
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SEQUENCE, 11 unordered piece
AC018497
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51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Yang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 3.9;
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of 31864 bp
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                                                                                                                                                                  Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihowa, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connot, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiltev, H., Viel, R., VO, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zalnoun, J., Zimmer, A. and Zody, M.
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                                                 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 31, 2000 this sequence version replaced gi:7280316. All repeats were identified maior personnel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boguslavkly, L., Boukhgalter, B., Brown, A., Bulkett, G., Collin Campoplano, A., Castle, A., Cheepel, Y., Colangelo, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, E
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-24K7
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                    repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
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/db_xref="taxon:9606"
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ns clone RP11-24K7,
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gap of unknown length
188432: contig of 45537 bp in
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Pred. No. 3.9;
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SEQUENCE, 18 unor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 4.6 in Q20 bases; Quality coverage: 4.5 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 140190 bases at least Q40 Consensus quality: 144274 bases at least Q30 Consensus quality: 145694 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 24_K_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 145000; agarose-fp
Insert size: 146569; sum-of-contigs
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                                       vector_side:left"
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                                                                                                                                                                              /organism="Homo sapiens"
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'note="assembly_fragment"
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21849: contig of 1049
21949: gap of 100 bg
                                                                                                                                                                                                                                                                                                                                                                                                                                        78837: gap of 100 bp

89917: contig of 11080 bp in length

90017: gap of 100 bp

100805: contig of 10788 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29864: gap of 100 bp
35579: contig of 5715 bp in length
35679: gap of 100 bp
41577: contig of 5898 bp in length
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29764: contig of 4060 bp in length
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147978: contig of 15246 bp in length
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47413: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13: gap of 100 bp
54860: contig of 7347 bp in length
160: gap of 100 bp
61589: contig of 6629 bp in length
189: gap of 100 bp
68215: contig of 6526 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1564: contig of 1564 bp in length is gap of 100 bp 20700: contig of 19036 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15: gap of 100 bp
18737: contig of 10422 bp in length
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contig of 17843 bp in length
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contig of 5736 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                      aaaacccttataaaacgogggttttcgcagaaacatgcgctagtatcattgatgacaaca 146
                                                                                                                                                                                                                                                                                                                                        tggactaagcaaaagtgcttgtcccctg 174
                                                             Mammalia; Eutheria; Pr
1 (bases 1 to 162249)
Birren,B., Linton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
77; Conserv
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       ACO20682 162249 bp DNA HTG 19-JI
HOMO Sapiens clone RP11-24G18, WORKING DRAFT SEQUENCE,
                                                                                                                            Homo sapiens
                             Unpublished
                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT
                                                Homo sapiens chromosome,
                                                                                                                                                                         C020682.3 GI:9280776
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Pred. No. 5;
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                                                Nusbaum, C. and Lander, E. me, clone RP11-24G18
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Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 19, 2000 this sequence version replaced gi:6731246. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                     28868 28967: gap of 100 bp
28968 39639: contig of 10672 bp in length
39640 39739: gap of 100 bp
39740 48843: contig of 9104 bp in length
48844 48943: gap of 100 bp
48944 63260: contig of 14317 bp in length
63361 63360: gap of 100 bp
63361 83571: contig of 19211 bp in length
82572 82671: gap of 100 bp
82672 100593: contig of 19212 bp in length
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1598 1697: gap of 100 bp
1698 4621: contig of 2924 bp in length
4622 4721: gap of 100 bp
4722 8497: contig of 3776 bp in length
8498 8597: gap of 100 bp
14869: contig of 6272 bp in length
14870 14969: gap of 100 bp
14970 20957: contig of 5988 bp in length
20958 21057: gap of 100 bp
21058 2867: contig of 7810 bp in length
21058 2867: contig of 7810 bp in length
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Center clone name: 24_G_18
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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/clone="RP11-24G18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr10
RP11-63A2 is from the library RPCI-11.1
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-63A2 The true right end of clone RP11-809M12 is at 46921 in this sequence.
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                                                                                                                                                                                                                                                                                                                      8555. .8854
/note="LIMC/D repeat: matches 5313.
                                                                                                                                                                                                                                                                                                                                                                                      8233. .8517
/note="MLT1-INTERNAL repeat: matches
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                                              /note="L1M4 repeat: matches 2695.
10829 11016
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/db_xref="taxon:9606"
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note="L1MC/D repeat:
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te-"L1MC5 repeat:
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:e="HERVL repeat:
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11411. .11516
                                                                                   note="LIMC5 repeat:
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                                  'note="L1MC5 repeat: matches 7603. .7774 of consensus"
                                                                                                                                                                      'note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                             'note="12 copies 2 mer tc 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                   note-"MIR repeat: matches 50. .144 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7233. .17352
note="3 copies 40 mer 75% conserved"
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                                                                                                                                                                                                                                                                                                                                                  ote="MIR repeat: matches 3. .137 of consensus"
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repeat: matches 16.
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 .260 of consensus"
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  Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                            HOMO Sapiens chromosome 10 clone RP11-809M12, PROGRESS ***, in ordered pieces
                                                                       AL356952.17 GI:15020905
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                       HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="8 copies 6 mer tacaca 61011. 61054
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 1849. 62072. .62276
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/note="Alusc:
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44598 ..44892
/note="AluSg repeat: matches 1. .296 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MLT1A1 repeat: matches 1. .180 of consensus"
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50064. .50218
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52.0%;
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  Chordata;
Primates;
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                   71;
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AUTHORS
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Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 155711)
1 (bases 1 to 15711)
2 Hall.N., Quail,M., Rajandream,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
77; Conserv
                                                                                                                                                                                   malaria parasite P. vivax.
                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax telomeric
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Insert size: 167487; 12.8% error; agarose-fp
Quality coverage: 6.20x in Q20 bases; sum-of-contigs Quality
coverage: 6.96x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye; 97% of reads Chemistry: Dye-primer Big Dye; 2% of reads Consensus quality: 187525 bases at least Q40 Consensus quality: 187814 bases at least Q20 Consensus quality: 187920 bases at least Q20 Consensus quality: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2001 this sequence version replaced gi:14970342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: bA809M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by the finished sequence as soon as it
the accession number will be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 188026)
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34467 c 34626 g 57498 t
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/db_xref="taxon:9606"
/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone="RP11-809M12"
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                                                                                                                                                                                                                                                                                                                                                                                                 155711 bp
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52.0%;
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Pred. No. 5.
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Mismatches
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FEATURES
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-JUN-2000) The Sanger Centre, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pus, Hinxton, Cambridge CB10 1SA, UK
more information about this project
http://www.sanger.ac.uk/Projects/P_vivax
                                                                                                                                                        /translation="MTSISNFEDSCKLSAFIKSLDSSPQMQAVDIDSYLNSVKEEQKD
TVREIYSELESLYSSIARQEDNIKSFCCFYLMYWLNKQRKEKLINVBVDAMQVIEKLW
GTLKNPSVSCKROHYYEPSVDKEKCVDLMVYCVNTDELQKHCEKPDQAEFKSTYCDNF
KKYTHIYYTYFTINVKCLRDYNNDIHPNWKFSDTCTHLDMAKTPFKYETSSQTIVDDG
TREKIRKCESHEDSRPINCYMLDGVPVTLEELSATINVIPLKYGIYAGSSFIGFISLG
LYLYKKTRHPSLVRTNSSRENKINKNTDKKLSHEKEKKSNSKNKDYKFSYNPIQN"
join(16650..16682,16811...17680,17800...17964)
/gene="vir4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="vir2, putative transmembrane protein, similar to vir1: MW:36805 (312 aa) fasta scores: opt: 380, E(): 0.00049, 28.0% identity in 296 aa overlap, and to vir9: MW:34499 (294 aa), fasta scores: opt: 377, E(): 0.00053, 27.2% identity in 290 aa overlap"
rpc subfamily, similar to rpc3, vir14: MW:40917 (348 fasta scores: opt: 878, E(): 8.4e-16; 42.1% identity 349 aa overlap, and to rpc1, VYIVD10.04: VYIVD10.tab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vir3, rpa1, putative transmembrane protein, member of rpa subfamily, similar to rpa2, pseudogene 5', vir31: MW:26193 (221 aa) fasta scores: opt: 862, E(): 8.2e-16, 55.5% identity in 218 aa overlap and rpa2, pseudogene 3', and to rpa3, vir17 MW:46668 (406 aa) fasta scores: opt:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /yene="vir3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="vir3"
/gene="vir3"
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SVIPLISLVTVLSVPTFFFILYKLTPFGAWFRDRSKGNKKNYSNIANEEPENLHASRI
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to vir33: MW:35552 (301 aa) fasta scores: opt: 437, E():
0.00013, 26.5% identity in 302 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB96692.1"
/db_xref="GI:8953644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRMSDIKTYKISYMSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKSTFNLNCKKSLNYLEYLEESEHTDIRKSQGTLYLYLWLYDKELKNVKNKGKHIDLY
NNLLELCFEYISYNIGTIYQSNVRADNFEILKNLYDLYYKFDKIKYDNDCENTKYKCA
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/gene="vir2"
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Y LNAVSYAV I AVFT LP I LSS I VFLLYKFT PLQSWI RPQ I VEKKKLLKNLQEETFKLQE
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FNDMISVYKEQMSSKINICĻNNMKYINNNVLKDLKILMDLFGNFNKFKEINKEKETDC
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/db_xref="GI:8953642"
/translation="MADETYNDSFKYVISFPKNKEYYESVTPSSDRTIVSACNQIRSK
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/qene="vir1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB96691.1"
/db_xref="GI:8953643"
/translation="MGGESMYHFSNRSYEHESLFLLNNTKVNQGHDHICEKFMSAYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=:
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/db_xref="taxon:5855"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      E(): 1.9e-06,
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                                                                              , rpc2, putative membrane protein,
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                                                         rotein, member
MW:40917 (348
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/note-"vir7, rpf1, putative transmembrane protein, member of rpf subfamily, similar to rpf2, vir29: MW:42155 (362 aa) fasta scores: opt: 805, E(): 1.4e-07, 39.88 identity in 374 aa overlap, and to rpf3, vir27: MW:42372 (362 aa) fasta scores: opt: 487, E(): 0.0004, 26.98 identity in 37
                                                                                                                                        DSGLQKVFEKILKAMCYMYTKKRHKIFDSDMCKFFYYWLADILINNLNDNHFTSEVLI
                                                                                                                                                                                                                                                                                                         aa overlap"
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IYTNEDTRQQGEGVYEQPGTDKTRSGMFGGSSGFPRYITEVFGSVDPVPVVGVSGGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAGDHQDPGYISYKDYVNAKHEFKRTMNNRYPDNERFEKIINKI
NNESHKWNLKNKTFTTLHNVLANDLAFYGGMKHHYCRFINYWLNKEVQNINNHFDKSY
FPIFQKFSDEFSIIKTNKNDQRCNNYIFNLSHKTINIMDILYGLYDEYDKIKSHREDS
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GCKSKIYGQLYKSCKENYGDDLLLLIEKNVNSYLEDQKTYIESLSALEVWIFKAQSLFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNEYKNQVSVL/CRKYVSFFKKIKHNNRSYSNPQDHKKYPEYLNFWIRHQLELQSISKY
DRSVLYIHLKNNYPQFDKERELENKIYCINEKDYKSMNILYDLYKNYYGSLHEYKTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12087:13361 reverse MW:39223 (343 aa) fasta scores: opt: 597, E(): 5.7e-10, 44.7% identity in 351 aa overlap and to rpc4, VYIVD10.20: VYIVD10.tab 81364:82388 reverse MW:34896
SSEVEDSSSISTTSKYIANVASVAGIVIPSYLVYNFTPAGTWINRLFGRTPKMNHNTL
                                                                  KKYLQTYVNKYKELHGYCEVEKRSDTYCKEFHKHFSNKEHNLLSTWSCNLEGTKLQLN
                                                                                                 NLYRILNEAGAGKICDPINSYIDKDNFENIKLIFDYSEDYESYKLDLAIPNRSCNENY
                                                                                                                                                             /protein_id="CAB96696.1"
/db_xref="GI:8953648"
/translation="MAEILGDEKLEILPTKHNYYYLDNGYTFCEKDIFYNHAERKLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALFLLFRYTPLGTFFRGGRGRAHRIPRSFNGQFLGAFPDINEYNGGYIGYGPMDIPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYGSCDTFLSWASNHNYAIDKYYENTNLYQKFEEIKKLIDNLKESSSSSCIKSIYLHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vir28:(458 aa), fasta
26.3% identity in 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGKIRFAYQPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFGAMSRISPTVISTMLTPLSSIFRKEKKRRKIPLFFPERSINDVKNHNSKHMKAKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:8953645"
/translation="MTEKDYFGKLISVIETISSDFNSEKFYNYLNNYDDLNKYYPYCT
SLNPKSKDIKYTNLRILCAQLVKYLKTTYTTLNKGDLKYDDCILLNYWIYSRLVNILG
                                      LIGDNQGKVVEEAQIGKSSTGKERGAELKETKVEGRAQAEPPVLTASSLETGSSLMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="vir7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQVVKLREEEEARREAAEKQKRALEEA I REREEAEKRQHEQELKAEKELLQRQANNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB96695.1"
/db_xref="GI:8953647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="vir6, putative transmembrane protein, similar to
vir28:(458 aa), fasta scores: opt: 344, E(): 0.00048,
26.3% identity in 468 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSDYSSEKTTDSEDFNIGYKLVKTSTFSKPFGLPQIKGVNYKELNELIRLQYNMPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYFFQSFKENYDKCLYRCYFGHDSKLCDVMKIFRELYDKQKFPNIQNQCHITSYTSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /youn(20974. .21000,21140.
/gene="vir5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPATOTGNILLGVVATSITSGALYRFTPLGNMLRNGFGRNNHNMRNMHGGEYGLFDYA
PESYNPFTGGGEEHYIGYHPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDT I KNTLPY FDOMCPKYMNYVESHTSLFKY FKTLCSKSSDOCPEFY NECNOYDPNVV
LRTFSCNETMAKKKAEETSEKDKLQLQGGRSAGQEANHGMRTNPEFSSGGSHLTRDGT
                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="vir6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )oin(24943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB96694.1"
/db_xref="GI:8953646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 low similarity to other YYIVD10 CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEDKTVIAPIFGKLVRIWNSIVANPLYTSPYNKCMPDSIIPTQNDWRKRKELYDYCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(24943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MEEVEEEKDYDIFKDLDDYETIIHQVNREYSDEPQANFCDSITF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .24969,25109.
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                                                                                                                                                                                                                                                                                                                                     0.0004, 26.9% identity in 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .30638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .26551)
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                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                           atagatgtgaaaacccttataaaacgcgggttttcgcagaaacatgcgctagtatcattg 137
                                                                                                                                                                                                                                                                                        AGAAAAA 94506
                                                                                                                                                                                                                                                                                                                                                                              AAATTCATTATAAAATTTTATAAAACTCGGAATTCTTCAAGAAAAATATGCTATTGAAATAA 94513
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGGTTTTTTTGTAACATGAATCCTTATTGTCTGTTCTATATTCAGTGCATTCTTTGTT 94573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                     Drosophila melanogaster clone RP98-24A2, ***, 45 unordered pieces
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
                                                                                            AC023713.2 GI:6997283
                                                                                                                AC0237
                                                                                                                                                                                  AC023713
                                                               HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                   unordered pieces.
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/db_xref="GI:8953650"
/translation="Mapsevokoaylhykeifhdstsnyqiftsycsnyksylodsde
/translation="Mapsevokoaylhykeifhdstsnyqiftsycsnyksylodsde
NKCSSLESCESTICKY YILLEONHAISISEGCKFLYYMYDKYIENOSSGCNNLEFYK
RSSLESCESTICKY YILLEONHAISISEGCKFLYCAGPDKLINSGDNEEPNKCAYA
RASLKSYCENGOWEECNNFVEOLDVHLEEKYNNLIVLCEQFDKLINSGDNEEPNKCAYA
KKCVELYEKYIKECLGGVNNYYCNELKRFKHDYEKKIKELTCADIATILTSSEETDLA
SIIIVPVIIIPALCFIYYIVNKFTPPGSWLSLRMYRKKNKYSNIENVTQKYIHSPKPT
EGNFQNRPYNVSYNSGOY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="vir10, rpd2, putative transmembrane protein, start unclear, member of rpd subfamily, similar to vir35, rpd1: (288 aa) fasta scores: opt: 1328, E(): 0, 70.2% identity in 292 aa overlap, and to rpd3, vir11: MW:25866 (218 aa) fasta scores: opt: 390, E(): 8.7e-15, 34.0% identity in 206 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vir9, rpg2, putative transmembrane protein; similar to vir15:MW:36805 (312 aa) fasta scores: opt: 398, E(): 0.00012, 26.0% identity in 289 aa overlap, and to vir2: MW:35019 (292 aa) fasta scores: opt: 377, E(): 0.00026, 26.1% identity in 287 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(40530. .41207,41326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(40530. .41207,41326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(37501..37539,37698..38378,38507..38671)
/gene="vir9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVLGFLYKFTPARSWFHGRNRGVKANNFLDEGEINEMFHNNPNFENMESDNSNYNIGY
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EDFLLTEGSPDVVIPLLGDRSAIAHRRDGEKSIAESSFLSDPLKSKISTGIAVGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB96697.1"
/db_xref="G1:8953649".
/db_xref="G1:8953649".
/translation="MDLPLSQEIDKWKKDYPFLESVWKLFGEYNNDMYDFEETHYELC
DFIISDEPERGMNKYKHFCIKLLRNLWHASEITYNNNMSPSERCINLNKWLYFYRKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity to other VYIVD10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(37501
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/gene="vir8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="vir8, putative transmembrane protein, low similarity to other VYIVD10 CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="vir10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                             57861 bp
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ir9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 155711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                         SEQUENCING IN PROGRESS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibbs, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D.M., Adams, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 57861)
                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 57861)
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Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Oswal, G., Parish, B., Paxton, S., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasguez, L., Vinson, R., Vo, Q., Wahbah, M., Worley, K., Weinstock, G., Weinstock, I.R., Williamson, A., Morley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, W.
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Submitted (17-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Feb 18, 2000 this sequence version replaced g1:6984287.
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                                          Center project name: DRAC
Center clone name: RP98-24A2
Center clone name: RP98-24A2
Center clone name: RP98-24A2
Center clone name: RP98-24A2
Center clone name: M13; L08821
Chemistry: Dye-terminator Big Dye: 99% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 18819 bases at least Q40
Consensus quality: 30569 bases at least Q30
Consensus quality: 37643 bases at least Q30
Quality coverage: 0.6x in Q20 bases; sum-of-contigs estimation
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TGTATAATTTGACTCTATTTAAATTCTTCAGAAAAATTAAACTGACAACATTATTTACAA 143991
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                                                               67;
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Submitted (01-7UL-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 1, 2000 this sequence version replaced gi:7711296.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.7% of Sequence; Estimated Total Number of Errors is 2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (16872)

DOE Joint Genome Institute and Stanford Human Genome Center.
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AC008554
AC008554:7 GI:8886966
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DOE Joint Genome Institute
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Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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12043 c 11927 g 15854 t 2455
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1. 179393
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On May 31, 2000 this sequence version replaced gi:7711484.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 179393) DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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AC010636
AC010636.6 GI:8122233
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.
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19 clone CTD-2332E11, complete sequence.
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Search completed: March 28, 2002, 15:16:11 Job time: 7935 sec

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
/SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 1 3 3 4 4 5 6 6 7 7 7 10 11 10 11 11	Result
33 33 33 34 34 34 34 34 34 34 34 34 34 3	Score
17.4 15.8 15.2 15.2 15.2 15.2 15.2 15.2 15.2	
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21 22 22 22 14 16 21 21 22 22 22	•
AAA64140 AAC27526 AAH5265 AAH54121 AAA46670 AAQ4834 AAQ90112 AAC78077 AAQ48935 AAC18077	ID
Nucleotide sequenc Human secreted pro S. epidermidis ope S. epidermidis gen cDNA of differenti hOSF-2pl. Homo sa TCI gene. Homo sa Human Cancer assoc hOSF-2os. Homo sa Human OSF-2 (perio Human bone marrow	Description

New beta-tubulin antigen in the membranous structure of the inner ear, reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from other autoimmune ear diseases

from other

WPI; 2000-558400/51

.2 14.	27.4 14.3	.4 14.3	27.4 14.3	41 27.4 14.3	27.4 14.3	39 27.4 14.3	38 27.4 14.3	37 27.4 14.3	36 27.4 14.3	35 27.4 14.3	34 27.4 14.3	27.4 14.3	27.6 14.4	27.6 14.4	.4	27.8 14.5	28 27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	27.8 14.5	19 28 14.6	28.6 14.9	29 15.1	16 29 15.1	29	14 29 15.1	29.2 15.2	7.CT 7.67
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AAC47825	AAT58840	AAH68531	AAS07063	AAF67831	AAH67361	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254	AAF58252	AAH84040	AAA78542	AAC45504	AAA78563	AAS21771	AAV71738	AAV71729	AAH54373	AAC33162	AAC43114	AAC48453	AAQ78141	AAH52400	AAS21896	AAH18508	AA163695	AAF28549	AAD05171	AAH34227	AAC74426	AAD02697	AAH72618
Arabidopsis thalia -	Mycoplasma genital	C glutamicum codin	DNA encoding Group	Corynebacterium gl	C glutamicum codin .	Oligonucleotide Dl		Oligonucleotide D2			Oligonucleotide D1	Eulemar rubrivente	Plant SDF polynucl	Arabidopsis thalia	Plant SDF polynucl	Human gene for col	Upstream sequence	Upstream sequence	S. epidermidis gen		Arabidopsis thalia	Arabidopsis thalia	Staphylococcus epi	S. epidermidis ope	Human collagen gen	Human cDNA sequenc	Human kidney relat	-	Human secreted pro		secreted	glycosyl	Human cervical can

ALIGNMENTS

RESULT

AAA64	AAA64140/c
X ₽	AAA64140 standard; DNA; 50000 BP.
AC	AAA64140;
XX	
ΡŢ	20-DEC-2000 (first entry)
×	
DE	Nucleotide sequence of a beta-tubulin antigen.
XX	
Χ¥	Beta-tubulin antigen; inner ear protein; Meniere's disease; autoantibody;
WW	chronic ear disease; autoimmune disease; ss.
XX	
SO	Homo sapiens.
×	
PN	W0200050593-A1.
XX	
PD	31-AUG-2000.
XX	
PF	25-FEB-2000; 2000WO-US04795.
X	
PR	25-FEB-1999; 99US-0121549.
XX	
PA	(UYTE-) UNIV TENNESSEE RES CORP.
X	
PΙ	YOO TJ;

Meniere's disease is a chronic ear disease with unknown etiology. Serum from patients suffering from this disease contain autoantibodies serum from patients suffering from this disease is believed to lan autoimmune disease. The beta-tubulin antigen is useful as a target substance in diagnosing or detecting Meniere's disease and in distinguishing this disease from other autoimmune ear diseases.

þe

The present sequence encodes a beta-tubulin antigen. The protein is an antigen of the membranous structure of the inner ear protein, and is reactive with antibodies from patients having Meniere's disease.

Claim 3; Page 74-97; 115pp; English

Query Match Best Local Matches

Local Similarity

17.4%; 52.5%;

Score 33.4; Pred. No. 0

DB ,.41;

Conservative

0;

Mismatches

66;

Indels Length 50000;

0;

Gaps

0

Sequence

50000 BP;

17281 A; 9480 C;

8791 G; 14448 T; 0 other;

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           The present sequence is one of a large number of 5' ESTs derived fiminals encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared total human RNAs or polyA+ RNAs derived from 30 different tissues sequences usually correspond mainly to the 3' untranslated region of the sequences of the sequences of the sequences.
                                                                                                 Claim 1; SEQ ID 31601; 71pp + CD-ROM; English.
                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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mRNA because they are often obtained from oligo dT primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag; chromosome mapping; ss.
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polypeptides may also be used to assay

inhibitors of their

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RESULT
AAH52605
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Best Local
           AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Stabhylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                         Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                                         WPI; 2001-316495/33
P-PSDB; AAG81755.
                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001
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                                                                                                                                                           Claim 8;
                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200134809-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                          Page 195; 2188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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51.0%;
                                                                                                                                                                                         polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain; infection; diagnosis;
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RRESULT
AAHS4121
ID AAHS4
XX AAHS
XX AAHS
XX AAHS
XX Stap
DT 03-5
XX Stap
XX Vacc
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAGB1454 to AAGB3120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55990 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention AAH55091 to AAH55998 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 1055-1056; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH54121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH54121 standard; DNA; 3204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1569 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity and therefore identify compounds that may be used treatment of S. epidermidis infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atatgaatatgaacaaaataatgagcgatccatatctctcactgcttataaaactaatgt 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taacgcggatatatttgatagtttgattaatgaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SR1 strain; infection; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1569;
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AAH53971
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2; tissue specific mRNA; insulin-like growth factor binding protein 6; OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDF1a; peripheral benzodiazepine receptor; annexin II cellular ligand; pl1; congenital heart failure; dilated congestive cardiomyopathy; opertrophic cardiomyopathy; restrictive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; mitral valve disease; aortic valve disease; tricuspid valve disease; pulmonary hypertension; arterial hypertension; renovascular hypertension; arterial arteriosclerosis; atherosclerosis; cardiac tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH55098 represent oligonucleotide sequences and primers which are use in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differentially expressed human gene; cardiac disease; kidney inflammatory disease; I-8U; prostacyclin-stimulating factor;
          Preventing, diagnosing and treating cardiac, kidney and inflammatory disorders using cardiac genes that are differentially expressed in disease states such as cardiac arrhythmia and arteriosclerosis -
                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA46670 standard; cDNA; 3077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA of differentially expressed human gene osf-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                            18-DEC-1998;
                                                                                                                                                                                                                          15-DEC-1999;
                                                                                                                                                                                                                                                                                          WO200035473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide sequences from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH55090 represent specifically claimed S. epidermidis genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 taacgcggatatatttgatagtttgattaatgaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 atatgaatatgaacaaaataatgagcgatccatatctctcactgcttataaaactaatgt 601
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DB; AAY93596.
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                                                                                                                                                            SCIOS
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                                                                                                                            White RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                            99WO-US29941.
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                                                                                                                              Damm
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Pred. No. 1
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                                                                                                                              Lewicki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990 T; 0 other;
                                                                                                                            JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                637
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                                                                                                                              Schreiner GF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory diseases associated with inappropriate expression of differentially expressed cardiac, kidney and inflammatory genes (e.g. AAA4668-79). These genes include I-8U, prostacyclin-stimulating factor, isf-2, tissue specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-1, YMP, BMC2, pre-B cell stimulating factor homologue (SDFla), peripheral benzodiazepine receptor, and cellular ligand of annexin II (pll), respectively. These diseases include congenital heart failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arterial hypertension, renovascular hypertension, arteriosclerosis,
                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA46668-79 represent differentially expressed human genes, associated with disease states and disorders. The specification describes methods preventing, diagnosing and treating cardiac, kidney and
WPI; 1993-304910/39
                                                                                                                                                  29-SEP-1993
                                                                                                                                                                             EP562508-A
                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                               Homo sapiens (placenta).
                                                                                                                                                                                                                                                                                                                                                         Bone-related protein; bone; diagnosis; disease; growth factor; cell adhesion; guiding; induction; metabolic bone disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ48934 standard; cDNA to mRNA; 3092 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3077 BP; 1032 A; 571 C; 632 G; 842 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis and/or cardiac tumours
                                                                                            27-MAR-1992;
                                                                                                                       22-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                    hOSF-2p1
                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-1994
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                           Tezuka
                                        Amann E,
                                                                  (FARH ) HOECHST JAPAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 attgcaacaaatggtgttgtcc 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            616 aaccattatcctaatggggttgtcactgttaattgtgctcgaatcatccatgggaaccag 675
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                                        Kikuno
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                                                                                             92JP-0071501
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102..2374
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38..101
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                                        Otawara-Hamamoto Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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RESULT
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Best Local Similarity
       The sequence is that of the TCI gene which encodes the TCI tumour marker protein. The gene and its product may be used to detect tumours in blood, urine or sputum. Inhibitors of TCI are used to treat late stage cancers and for preventing tumour cell metastasis See also AAQ90113-25.
                                                                                                      New tumour marker TC1, corresp. DNA and monoclonal antibody detecting, preventing and treating tumours, esp. in breast, and gastrointestinal tract cancer.
                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSF-2 plays an important role in the formation of bone, by acting as a growth factor or adhesion or "guiding" protein to attract cells to the site of bone induction. In a pharmaceutical compsn. it can
                                                                                 Disclosure; Fig 4; 84pp; English.
                                                                                                                                                                    WPI; 1995-178826/23
                                                                                                                                                                                          Bao S,
                                                                                                                                                                                                                                        29-OCT-1993;
                                                                                                                                                                                                                                                                                          04-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ90112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ90112 standard; cDNA; 3126 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3092 BP; 1035 A; 573 C; 638 G; 846 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the site of bone induction. In a position is to the applied in metabolic bone diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 14-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian OSF-2 protein - obtd. from diagnosis and treatment of metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR41868
                                                                                                                                                                                                                (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                                 31-OCT-1994;
                                                                                                                                                                                                                                                                                                                 WO9511923-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 aaccettataaaacgegggttttegeagaaacatgegetagtateattgatgacaacatg
                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attgcaacaaatggtgttgtcc 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gactaagcaaaagtgcttgtcc 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaccattatcctaatggggttgtcactgttaattgtgctcgaatcatccatgggaaccag 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                           Chen LB,
                                                                                                                                                       AAR74302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                          9305-0146488
                                                                                                                                                                                                                                                                 94WO-US12502
                                                                                                                                                                                                                                                                                                                                                                                                                invasive; metastatic; cancer;
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 43..2376
                                                                                                                                                                                          Liu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.2%;
59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone tissue, useful for bone disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                    - for
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Sequence 3126 BP; 1035 A; 611 C; 656 G; 824 T; 0 other;

DB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
          include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynuclectides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynuclectides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of
                                                                                                                                                                                  AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities
                                                                                                                                                                                                                                                       Claim 1; Page 1006-1007; 2352pp; English
                                                                                                                                                                                                                                                                                           Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antiatbettic; antiasthmatic; antirheumatic; antirhritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200055350-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer associated gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune disorder; haematopoietic cell disorder; autoimmune disorder;
allergic reaction; graft versus host disease; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC78077 standard; cDNA; 3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naemostatic;
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DB; AAB43868.
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                                                                                                                                                                                                                                                                                                                                                                                                 CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attgcaacaaatggtgttgtcc 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaccattatcctaatggggttgtcactgttaattgtgctcgaatcatccatgggaaccag 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124270
treat disorders of haematopoietic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%;
59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.2;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO:471.
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                                                                                                                                                                                                                                                                                                           peptides
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CCC CXXX PT XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                          Mammalian OSF-2 protein - obtd. from diagnosis and treatment of metabolic
                                                                                                                               Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytric activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78447 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                            P-PSDB; AAR41869
                                                                                                                                                                                                                                                                                       WPI; 1993-304910/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone-related protein; bone; diagnosis; disease; growth factor; cell adhesion; guiding; induction; metabolic bone disease; ss.
                                                                                                                                                                                                                                                                                                                                          Tezuka
                                                                                                                                                                                                                                                                                                                                                                Amann E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP562508-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ48935 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   (FARH ) HOECHST JAPAN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hOSF-2os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3202 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 gactaagcaaaagtgcttgtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 attgcaacaaatggtgttgtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                            Page 18-22;
                                                                                                                                                                                                                                                                                                                                                                   Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (osteosarcoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92JP-0071501
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95..2539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 32..2542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                         58pp; English.
                                                                                                                                                                                                                                                                                                                                                                Otawara-Hamamoto Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29.2; D
Pred. No. 3.7;
0; Mismatches
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                                                                                                                                                                             bone tissue,
bone disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         861 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                                                                                                                                                                                                                                                                                                Takeshita
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                                                                                                                                                                                                     useful
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OSF-2 plays an important role in the formation of bone, by acting a growth factor or adhesion or "guiding" protein to attract cells to the site of bone induction. In a pharmaceutical compan. it can be applied in metabolic bone diseases.

SS X

Sequence 3253 BP;

1106

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665 G;

883 T;

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other;

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RESULT 1
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Best Local S
Matches 49
                      The patent discloses methods of correlating gene expression with inflammatory diseases and renal disorders in healthy and disease samples. The invention specifically relates to methods which monitor the expression of OSF-2 (periostin). The OSF-2 proteins are useful as markers in renal diseases such as immunoglobulin A nephropathy (19AN). Modulators of OSF-2 are used to treat 19AN, glomerulonephritis, including mesangial proliferation; inflammation; necrotising crescentic glomerulonephritis (NCGN), minimal change disease and sclerosis. The present sequence is a cDNA encoding human OSF-2 (periostin) protein.
                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                          Claim 1; Page 46-50;
                                                                                                                                                                 New polypeptide encoding OSF-2 (periostin), useful disease, e.g., immunoglobulin A nephropathy
                                                                                                                                                                                                                                       Munger WE,
                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-0180136
                                                                                                                                                                                                                                                                                                              05-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                             WO200157062-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mesangial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD12765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD12765 standard; cDNA;
                                                                                                                                                                                                                                                              (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; OSF-2;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 attgcaacaaatggtgttgtcc 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
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                                                                                                                                                                                                                 2001-488865/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gactaagcaaaagtgcttgtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaccattatcctaatggggttgtcactgttaattgtgctcgaatcatccatgggaaccag 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSF-2; periostin; antiinflammatory; nephrotrophic; renal disorder; oglobulin A nephropathy; IgAN; glomerulonephritis; inflammation; glap proliferation; necrotising crescentic glomerulonephritis; minimal change disease; sclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                               GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
 3324
                                                                                                                                                                                                                                       Sun H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (periostin) cDNA
                                                                                                                                                                                                                                                               LOGIC
                                                                                                                                                                                                                                                                                                              2001WO-US03654
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 BP;
                                                                                                                                                                                                                                                                                                                                                                               /product-
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 33..2543
 1146 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.2%; 59.8%;
                                                                                                                                                                                                                                         Falk
                                                                                                                                         57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3324
                                                                                                                                                                                                                                         골
 809
                                                                                                                                                                                                                                                                                                                                                                                  "Human OSF-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
ç;
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 676
 G;
 894 T;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Query Match

15

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Score

29.2;

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22;

Length 3324;

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RESULT 11
AAH89937
ID AAH899
XX
AAH899
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DAH899
DT 01-OCT
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HUMAN
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PN W020
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PN 25-1
PR 30-1
PR 19-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ford JE, be, Wang;
                                                                      immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one
                          or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening
                                                                                                                                                                                                                                                                           expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ААН89937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH89937 standard; cDNA; 3405
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488707/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                               The present sequence is one of 251 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAM00818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 aaccattatcctaatggggttgtcactgttaattgtgctcgaatcatccatgggaaccag 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681 attgcaacaaatggtgttgtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                             treating e.g. cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gactaagcaaaagtgcttgtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                 Page 252-253; 648pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boyle BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0250583.
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Werhman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cytostatic;
erial; antifungal; anti-HIV; ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YT, Liu C, Asundi V,
F, Xu C, Xue AJ, Yan
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
                                                                                                                                                                                                                                                                                                                               polynucleotides
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Y, z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective;
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ng J;
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Query Match
Best Local Similarity
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Best Local Similarity
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                                                         The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic actis and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2618
                                                                                                                                                                         New
and
                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1491
                                          Sequence
                                                                                                                                                    Claim 1; Page 764-765; 1051pp; English.
                                                                                                                                                                                                                         Schlegel
                                                                                                                                                                                                                                                                           12-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                               21-DEC-1999;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                    08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                       08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                               WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cervical cancer marker nucleic acid 3892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH72618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH72618 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                       isolated nucleic acid for diagnosing and treating of assessing and detecting compounds for treating
                                                                                                                                                                                                      2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ga 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ga
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                                                                                                                                                                                                                                            MILLENNIUM PREDICTIVE
                                          3448
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2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                        Deeds J,
                                                                                                                                                                                                                                                                                                                                       2000WO-US33312.
                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                    99us-0169681
                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; pre-malignant condition;
                                         1164 A; 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 3448
                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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           22;
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myocarditis; adult respiratory distress syndrome; eczema; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyarteritis nodosa; polymyositis; systemic sclerosis; glomerulonephritis; myasthenia gravis; Sjogren's syndrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; glycosyl sulfotransferase-4; GST-4; immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human glycosyl sulfotransferase-4 (GST-4) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001
                                                                                                                                       intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; hypersensitivity; rheumatic fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                    /note= "Includes and all of 3'UTR" 47939..47955
                                                                                                                                                                                                          /number= 3
/label= 4a_5U2
45186..46633
                  /note= "Portion
47956..49128
                                                                                                                                    /number 4
/label 4a_5U1
46701..47938
'product= "Human glycosyl
                                                                                                                                                                                                                                             /*tag= d
45094..45185
/*tag= e
                                                                                                                                                                                                                                                                                                           /cons_splice=
35593..35674
/*tag= c
                                                                                    'number≔
                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
32847..32922
                                                                                                      cons_splice=7939..49746
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                                                                                                                                                                              cons_splice=6634..46700
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2923..35592
                                                                                                                                                                                                                                                                          label= 4a_5U3
5675..45093
                                                                                                                                                                                                                                                                                                                                                                            number=
                                                                                                                                                                                                                                                                                                                                                                                      *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 160552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       739
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                                                                                                                 (5'site:YES,
                                                                                                                                                                                         (5'site:NO,
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                                σį
                                                                          base
                                untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sjogren's syndrome; adrenalitis;
                                                                       pairs
transferase-4alpha
                                                                                                                                                                                            3'site:NO)
                                                                                                                                                                                                                                                                                                                                3'site:YES)
                                                                                                                 3'site:NO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue rejection;
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                                                                          of 5'UTR,
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                             region (5'UTR)"
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therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SIE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, adermatitis, myocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection during transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'UTR
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                                                                                                                                                between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sg
                                                                                                                                                                                                  GST is a type
                                                                                                                                                                                                              chromosome 16q23.1
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13-JUL-2000;
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                                                                                                                                                                                                                                                             Example 1; Page 62-104; 128pp;
                                                                                                                                                                                                                                                                                                  New glycosyl sulfotransferases
                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intro
                                                                                                                                                                                                                        present sequence is encoding GST-4alpha
                                                                                                                                                                                                                                                                                                                           2001-138471/14.
DB; AAY72639, AA
                                                                                                                                                                                                                                                                                     and therapeutic agent screening applications
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144694.
2000US-0593828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US19741
                                                                                                                                                                                                 membrane protein useful for inhibiting a binding event
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/cons_splice=
98457..99968
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96413..96484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8474..99661
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                                                                                                                                                                                                                                                                                                                            AAY72640
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485..98456
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                                                                                                                                                                                                                        human glycosyl sulfotransferase-4 (GST-4) and GST-4beta. GST-4 gene is found on
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                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                             (GST)-4alpha, GST-4beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyl transferase-4beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'site:NO)
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Query Match

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Score 29.2;

ВВ

22; Length 160552;

Sequence

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G; 44564 T;

119 other

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RESULT 14
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ID AAC744
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XX Human;
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                       and vulnerary. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include pathological condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding 50 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives \cdot
                                                                                                                                                                                              antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
                                                                                                                                                                                                                                                               The polynucleotide sequences given in AAC74396 to AAC74445 encode the human secreted proteins given in AAB40151 to AAB40200. AAB40201 to AAB40236 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999;
07-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; angiogenesis, autoimmune disease; hyperproliferative disorder; infection; skin aging; cardiovascular disorder; cerebrovascular disorder; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 31 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 324; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-594645/56
DB; AAB40181.
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2000US-0174871.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM,
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0; Mismatches
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RESULT 15
AAH34227/C
ID AAH342
XX Human
XX Human
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XX O5-APR
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XX AAH32
CC CANCEL
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Best Local
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AAH34227 standard; cDNA; 1444 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. AAC74387 to AAC74395 and AAB40150 represent sequences used the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                           cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colo cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer;
colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides; useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, cerebrovascular disorders, angiogenesis, nervous system
                                                                                                                                                                                                                                                                                 AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3046; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ААН34227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AATAATATAGGAAATCTCTGTTAAAGCACTGCTCGCCGTGAAGTAATGGAAGAGAGTCAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 CATTGACTACATATAATAAGAAAAATAGTTTTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 amatagatgtgammacccttatammacgcgggttttcgcagmmaccatgcgctagtatcat 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2001-235357/24.
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53; Conserv
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99US-0163280.
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; ss.
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Pred. No. 2.5;
0; Mismatches
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2.5;
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Search completed: March 28, 2002, 15:15:31 Job time: 7115 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1444 BP; 487 A; 202 C; 227 G; 527 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
                                                                                                                                                                                                          116
                                                                                                                                176
                                                                                                                                                                       131
                                                                                                                                                                                                                                                191 TATTACTGAAACCTTCCATACTACAGAAGTGCTGTACTTTTAAAATATTAAGTTTACAAA 132
                                                                                                                                                                                                                                                                                                                      Local Similarity hes 65; Conserv
                                                                                                                                                                                                                                                                    56 tattttcaataccttcggggaaatagatgtgaaaacccttataaaacgcgggttttcgca 115
                                                                                             71 TCAAA 67
                                                                                                                                                                                                    gaaacatgcgctagtatcattgatgacaacatggactaagcaaaagtgcttgtcccctga 175
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Pred. No. 3.1;
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Result
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length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2
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  Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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            US-08-204-288-3

US-08-188-582-12

US-08-646-715-12

US-08-646-715-12

US-08-530-5248-1

US-08-747-2218-30

US-08-747-2218-32

US-08-747-2218-32

US-08-747-2218-32

US-08-747-2218-24

US-08-747-2218-24

US-08-747-2218-24
                   US-08-747-221B-24

US-08-747-221B-26

US-09-05-051-26

US-09-005-051-26

US-09-005-051-26

US-08-222-719-7

US-08-471-613-7

US-08-471-613-7

PCT-01593-10443-7
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US-08-477-396A-3
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US-08-426-627-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
ORIGINAL SOURCE:
            MOLECULE TYPE:
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                       TOPOLOGY: 11
                                                          LENGTH:
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13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.2	13.2	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3
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Sequence 1, Appli	Sequence 1, Appli	Sequence 64, Appl	Sequence 63, Appl	Sequence 64, Appl	`	Sequence 65, Appl	Sequence 65, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 43, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 50, Appl	•	Sequence 50, Appl

ALIGNMENTS

GENERAL INFORMATION: APPLICANT: Amann, 1 APPLICANT: Otawara APPLICANT: Kikuno, Sequence 3, Application US/08426627 Patent No. 5756664 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/036,84 FILING DATE: 25-MAR-1993 APPLICATION NUMBER: JP 4-71501 FILING DATE: 27-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: Hammond, Alan W. REGISTRATION NUMBER: 35,178 REFERENCE/DOCKET NUMBER: 02481-1 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/426,627 TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000 TELEFAX: 202-408-4400 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: No. 5756664el Protein with Bone Formation TITLE OF INVENTION: Ability and Process for Its Production. NUMBER OF SEQUENCES: 24 ADDRESSEE: Finnegs ADDRESSEE: Dunner STREET: 1300 I Sta CITY: Washington FILING DATE: CLASSIFICATION: 435 TYPE: nucleic acid 20005-3315 3092 base pairs 1300 I Street, N.W. Otawara-Hamamoto, Kikuno, Reiko Takeshita, Sunao Tezuka, Kenichi linear Amann, Egon Finnegan, Henderson, Farabow, Garrett Dunner CDNA to mRNA double Release #1.0, Version #1.25 US 08/036,841 US/08/426,627 ω 02481-1285-00000 Yoko

FEATURE

ORGANISM: H

Homo sapiens E: Placenta

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; NAME/KEY:
; LOCATION:
US-08-426-627-3
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                                                                     TELEFAX: (617) 451-0313 NFORMATION FOR SEQ ID NO:
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tent No. 5872235
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                       SEQUENCE CHARACTERISTICS:
                                                                                                     REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                     FILING DATE: 28-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12502
FILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF INVENTION: ISOLATING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICATION NUMBER: US ...
TWG DATE: 29-OCT-1993
TWGER: US 08/448,388
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS:
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                                   ENGTH:
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                 nucleic acid
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                                 3126 base pairs
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Liu, Yuan
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join(101..2375)
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Pred. No. 1

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; LOCATION:
US-08-477-396A-3
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Best Local Similarity
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                                                                              TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3253 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
                   MOLECULE TYPE:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Hammond, Alan W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                              STRANDEDNESS:
                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 25-MAR-1993 APPLICATION NUMBER: JP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                  NAME: Hammond, Alan W
REGISTRATION NUMBER: (
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                                TOPOLOGY:
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                                                                                 3253 base pairs
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43..2376
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                                linear
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                   CDNA to mRNA
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Pred. No. 1;
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; NAME/KEY:
; LOCATION:
US-08-426-627-5
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Best Local Similarity
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 128, Application US/08943731
                  TELEX: 831-494
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Relication DATA:
                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
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SEQUENCE CHARACTERISTICS:
                                                                                                                               APPLICATION NUMBER: US 07
APPLICATION NUMBER: US 07
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                               TELEFAX:
                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                   215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KORKKO, JARMO
ALA-KOKKO, LEENA, et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLIGE, ALAIN EARLY, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEREDA, LARISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROCKOP, DARWIN J. SPOTILA, LORETTA D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELTAS, CONSTANTINOS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARSON, ANDREA W
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join(97..2540)
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join(32..2540)
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59.8%;
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                                                                                                      36,317
                                                                                                                                                                                         US 07/803,628
                                                                                                    9598-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.5%;
Best Local Similarity 65.1%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                    TELEFAX: 317-276-1294 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/330,154
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/208,925
FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TITLE OF INVENTION:
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3169
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                                  FEATURE:
                                                  MOLECULE TYPE:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
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NAME/KEY:
                                                                                                                                                                                                                     NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                STRANDEDNESS:
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                                                                                                                ENGTH:
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                                                                                                nucleic acid
                                                                                                                1257 base pairs
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Skatrud, Paul L
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                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/330,154
27-OCT-1994
                                                DNA (genomic)
                                                                                  double
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                                                                                                                                                                                                                                                                                                             US/08/057,163
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Pred. No. 1
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89 aaccettataaaacgegggttttegeagaaacatgegetagtateattgatgacaacatg 148

Query Match

Local Similarity

Conservative

14.5%;

Score 27.8; | Pred. No. 2.2); Mismatches

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2.2;
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Length 1257;

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Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/943 77
FILING DATE: 03-007
                                                                                                                              TELEX: 831-494
NFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 24183 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
ADDRESSEE: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
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APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                     TOPOLOGY:
                                                  TYPE: nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PHILADELPHIA
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                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/212,322
                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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                                                                      nucleic acid
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                 DNA (genomic)
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                                                      double
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RESULT 7
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TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
LINKAGE SIGNAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08204288 Patent No. 5959178
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Best Local Similarity
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Best Local Similarity
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 837 agtaattacaacatgtattgtgc 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777 ggaagtgtctgtaaaacgggttacaagacacagatatgcacttatacccataccattagc 836
                                                                                                                                                                STREET: Live No.
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FILING DATE: 10-APR-1989
   APPLICATION |
FILING DATE:
                                                                                                                                        COUNTRY:
                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1009
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                                                                                                                           2: D.C.
TRY: U.S.A.
20005-3518
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                                                                                                                                                                                       E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                          JOUANIN, Lise
KNIGHT, Mary E.
                                                                                                                                                                                                                                                                             VAN MONTAGU, Marc
LEGRAND, Michel
                                                                                                                                                                                                                                                                                                                                            INZE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            FRITIG, Bernard J.M.
                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                         VAN DOORSSELAERE,
MBER: US/08/204,288
10-MAR-1994
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57.8%;
                                                                                                                                                                                                                                                                MODIFICATION OF LIGNIN SYNTHESIS
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65.1%;
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 Mismatches

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Pred. No. 7
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FILING DATE: 10-SEP-PRIOR APPLICATION DATA:

10-SEP-1991

GB 9119279.9

APPLICATION NUMBER:

CLASSIFICATION: 800 PRIOR APPLICATION DATA:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
                                                                                                                                            ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-CAN-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB92/01460 FILING DATE: 09-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 attitcaataccitcggggaaatagatgtgaaaacccitataaaacgcgggitttcgcag 116
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                  STATE:
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NAME: Osman, Richard A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Tanese, Naoko
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62.78;
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-418/
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
APPLICATION NUMBER: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
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LENGTH: 3182 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TATA-BINDING PROTEIN AS
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                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/646,715 FILING DATE: 09-MAY-1996 CLASSIFICATION: 435
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STRANDEDNESS: doub
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                                                                                                        REFERENCE/DOCKET NUMBER:
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39; Conserv
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Weinzierl, Robert O.J.
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972..3002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATA-BINDING PROTEIN ASSOCIATED FACTORS,
NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                           36,627
ER: A-
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Pred. No.
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; LOCATION:
US-08-646-715-12
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                                                     Best Local Similarity
Matches 51; Conserv
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Best Local Similarity
Matches 39; Conserv
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REÀDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,683
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3852 base pair
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                      TOPOLOGY: 1
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                                                                                                                                                        NAME/KEY:
LOCATION:
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CITY: Bloomfield Hills
75 gaaatagatgtgaaaacccttataaaacgcgggtttttcgcagaaacatgcgctagtatca 134
                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: September 15,
CLASSIFICATION: 435
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STRANDEDNESS: double
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                                                       Conservative
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Conservative
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972..3002
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                                                                   Score 27; DB 1; Length 3852; Pred. No. 6.5;
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                                                     Mismatches
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                                                   Indels
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RESULT 13
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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (810)641-0270 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                       3627 TTTTAAAAAACACTGATTAATTATAATTGCT 3657
                                                                                                                                3567 GATTTGCATGTGATGAGCCTGGCAGCAAAGTGGTATTGCCTTTAACTTGAGATTGAACCA 3626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36,683
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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ADDRESSEE: Harness, Dickey & Pierce, P.L.C
STREET: P.O. Box 828
                                                                                         135 ttgatgacaacatggactaagcaaaagtgct 165
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TITLE OF INVENTION: Bovine
TITLE OF INVENTION: Of Use
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                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                          y Match 14.1%;
Local Similarity 56.0%;
hes 51; Conservative
                                                                                                                                                    75 gaaatagatgtgaaaacccttataaaacgcgggttttcgcagaaacatgcgctagtatca 134
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: Septem CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Bloomfield Hills
STATE: Michigan
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TD NO: 1:
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Jones, Margaret
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US-09-347-803-19

Sequence 19, Application US/09347803 Patent No. 6274379 GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

PPLICANT: Hitz, Bill PPLICANT: Kinney, Tony PPLICANT: Orozco, Buddy

[TLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes

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80
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Best Local Similarity
Matches 31; Conserv
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CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1022
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Silver, Gary W
APPLICANT: Wisnewski, Nanc
                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                            NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                  FILING DATE: NO CLASSIFICATION:
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                                                                                  STRANDEDNESS:
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Heska Corporation
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NN: 435
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Pred. No. 8.8;
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US-08-747-221B-32
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                   TOPOLOGY: 1.
MOLECULE TYPE:
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NAME: Verser, Carol Talkington
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APPLICANT: Wisnewski,
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CITY: Fort Collins
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Pred. No. 11;
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Pred. No. 11;
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Search completed: March 28, 2002, 15:10:40 Job time: 7484 sec

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Perfect score:
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Gapop 10.0 , Gapext 1.0
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BG542199
AZ964979
CNS0757U
AQ017410
AQ0168787
AZ931427
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                                          BH039236 RPCI-24-2
BG542199 602571637
AZ964976 ZM0234D24
AL435288 T3 end of
AL425760 clone BA0
AQ017410 CTT-HSP-2
AQ268787 RPCII1-74
                                                                                                              Description
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L0959C09-
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ALIGNMENTS

FEATURES	TITLE JOURNAL COMMENT	Z .	LOCUS
Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pde)ong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 254 row: N column: 24 Seq primer: T7 Class: BAC ends. Location/Qualifiers	Loses I to 749) Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-254N24.TJ	, DNA sequence. BH039236 BH039236. BH039236.1 GI:14816964 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	BH039236 749 bp DNA GSS 17-JUL-2001 RPCI-24-254N24.TV RPCI-24 Mus musculus genomic clone RPCI-24-254N24

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RESULT
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73; Conserv
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602571637F1 NIH_MGC_77 Homo
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Plate: LLCM1522 row: j column: 10
                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                               ound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: CLONTECH Laboratories, In CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Location/Qualifiers
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/clone_lib="NIH_MCC_77"
/clone_lib="NIH_MCC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcggcc); Site_2: SfiI (ggcgattatggcc); 5' adaptor
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-254N24"
/clone_1ib="RPCI-24"
                                                                                                                                  /clone="IMAGE:4696041"
                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0234 row: D column: 24
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
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Islam, H., Longacre, S.,
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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801 585 7177
                                                                                                                                                                                                                                                                 quality sequence stop: 600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
                                      Laboratory Mouse DNA Resource
                                                    /note="Vector: PWD42nv; Purified genomic musculus C57BL/6J (female) was obtained
                   (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                            /lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                  /sex="Female"
                                                                                                                                               /clone-"UUGC2M0234D24"
                                                                                                                                                                                     /strain-"C57BL/6J"
                                                                                                                                                                                                         /organism="Mus
                                                                                                                                 clone_lib="Mouse 10kb plasmid UUGC2M library"
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hydrodynamically sheared by repeated passage through
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Pred. No. 1
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RESULT 4
CNS079HE/c
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              Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mall: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii. Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia servitohilla
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T3 end of clone BBOAA029A02 of library BBOAA from of Pichia angusta, genomic survey sequence.
AL435288
AL435288.1 GI:12218701
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FEBS Let
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                                                                                                                                                                                                                                                                                                                                                                     Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Souclet, J.L., Algle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montign, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                          Genoscope.
Direct Submission
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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1 (bases 1 to 945)
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefigenoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                             Genomic exploration of the hemiascomycetous yeasts: 1. yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
Kluyveromyces lactis
PERG 1941
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Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1. (bases 1 to 845)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                 Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fikuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                   Wincker, P. and Weissenbach, J
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett.
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                                                                                                                                      Genoscope
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HAS1; helicase associated with
j putative frameshift(s)"
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Pred. No. 2
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SOURCE
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                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                   Unpublished (1998)
Other_GSSs: CIT-HSP-2306D3.TR
Contact: Mark Adams
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                              end search page:
                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                      Building
                                                                                                                                                                                                                                                                                                                       Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                              Simon, M.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
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RPA135 ; DNA-directed RNA polymerase I, 135 KD subunit
/evidence=not_experimental
155 c 154 g 260 t 2 others
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/clone="BA0AB033E09"
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/strain="CLIB 210"
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3.TF CIT-HSP Homo sapiens genomic clone 2306D3,
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Pred. No. 3.2;
""smatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       library availability, please contact Pieter de Jong (pieteredejong.med.buffalo.edu). Clones may be purchased from
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                                                                                                                                                                                                                                                                                                                                                                                                                   mail: mdadams@tigr.org
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                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:7528359"
/db_xref="taxon:9606"
/clone="RPCI-11-74N16"
/clone_lib="RPCI-11"
                  /note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
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/clone="2306D3"
                                                                        /sex="Male"
/cell_type="Lymphocytes"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements becomparative DNA sequence analysis
Unpublished (2001)
Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces unisporus
Saccharomyces unisporus
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Eukaryota; Fung1; Ascomycotaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Box 8232, 4566 Scottel: 314 362 2735 Fax: 314 362 7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unisporus genomic clone
AZ931427
AZ931427.1 GI:13502338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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/strain="NRRL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
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/clone=lib="Saccharomyces unisporus NRRL Y-1556"
/note="Random genomic sequence"
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54.5%;
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Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
BG062885 552 bp mRNA EST L0959C09-5 NIA MOUSE Newborn Kidney cDNA Library2 musculus cDNA clone L0959C09 5', mRNA sequence. BG062885 GI:12533811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovenome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Ouetler, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Location/Qualifiers
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Roest-Crollius, H.,
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/db_xref="taxon:99883"
/clone="123G15"
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/note="Genoscope sequence
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Billault,A., Quetier,F., Saurin,W., Bernot,A. and
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GSS; genome survey sequence. Tetracdon nigroviridis. Tetracdon nigroviridis Tetracdon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Euteleostei; Neoteleostei Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
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niaEST (http://lgsun.grc.nia.nih.gov/cDNA/cDNA.html)
Plate: L0959 row: C column: 09
Seq primer: -21M13 Reverse
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Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: George J. Kar
Laboratory of Genetics
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Mammalia; Eutheria; Rodentia;
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Site_1: Sall; Site_2: NotI; Cloned unidirectionally
Oligo(dT)-NotI Primer:
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/clone="L0959C09"
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Pred. No. 6.1;
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        leostei; Neoteleostei;
Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTGAGATAGGTCAAAAACAACATTCCTGTCTAACTTAACAAAGGAAGAGTTTGATTATT
                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                   114), genomic survey sequence.
AL067468
AL067468.1 GI:4946030
                                                                                                                                                                                                                                                                                                                                           GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BACR15P04 of RPCI-98 library from Drosophila melanogaster /forter

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila

                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o scale clone-end sequencing project of the Tetraodon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bernot, A., Fizames, C., Winc. Saurin, W. and Weissenbach, J
                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                   fruit fly,
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1 (bases 1 to 958)
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/clone_lib="G"
/note="Genoscope sequence
200 c 211 g 272
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/db_xref="taxon:99883"
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Pred. No. 6
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2 others
Genome Project (BDGP).
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                     out as
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PUBMED
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                                                                                              PUBMED
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                                                                                                                                   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Konno,H., Akiyama,J., Nishi,K.,
Sumi,N., Ishii,Y., Nakamura,S.,
                                            Shibata, K.,
                                                                                                                                                                                                                                                                                                                                   Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (strain:C57BL/6J) adult female placenta cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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Mus musculus adult fe
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  (bases 1 to 2062)

The R., Itoh, M., Aizawa, R.,

The J., Nishi, K.,
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/clone_lib="RPCI-98"
/clone="BACR15P04"
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/db_xref="taxon:7227"
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Pred. No. 7;
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Sciurognathi; Muridae; Murinae; Mus
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                      Nagaoka, S., Sasaki, N.,
Kitsunai, T., Tashiro, H
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Hazama, M.,
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                                          Carninci, P.,
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/protein_id="BAB24034.1"
/db_xref="GI:12837992"
RDHFGSKHPKYSDTLLDYGFYLLNVDNICQSVAIYQAALDIRQSVFGGKNIHVATAHE
                                                              RAVECCVRLLHVRNGNCKYHLGEETFKLAQTYMDKLSKHGQQANRAALYGELCALLFA
KSHYDEAYKWCVEAMKEITAGLPVKVVVDVLRQASKACVVKREFKKAEQLIKHAVYLA
                                                                                                                                                                                                  /translation="MAAVELEWIPETLYNTAISAVVDNYIRSRRDIRSLPENIQEDVY
YKLYQQGRLCQLGSEFCELEVFAKVLRALDKRHLLHHCFQALMDHGVKVASVLAYSFS
RRCSYIAESDAAVKEKAIQVGFVLGGFLSDAGWYSDAEKVFLSCLQLCTLHDEMLHWF
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/db_xref="MGD:MGI:1895310"
/db_xref="MGD:MGI:1914134"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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18. .1775
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1 (bases 1 to 2366)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sughhara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome research. 10 (10), 1617-1630 (2000)
 Adachi, J., Aizawa, K., Akahira, S., A
Arakawa, T., Carninci, P., Fukuda, S.,
                                                        Nature 409, 685-690 (2001)
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Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae;
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Fukunishi,Y., Furu
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                                                            sapiens (
                                                                       AQ787593 510 bp DNA GSS 03-AUG-1999 HS 2239_B1_F02_T7C CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate-2239 Col-3 Row-L, DNA sequence.
                                         AQ787593.1 GI:5695217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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555 c 604 q
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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/db_xref="MGD:MGI:1895026"
/db_xref="MGD:MGI:1914134"
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/strain="C57BL/6J"
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                                                                                                                145 catggactaagcaaaagt 162
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 510)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 510.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2239 row: L column: 3
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E-Col1 DH10B"
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/sex="male"
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/db_xref="taxon:9606"
/clone="plate=2239 Col=3 Row=L"
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION							DEFINITION	Locus	AF105113	RESULT 1
Comparative genetics of capsular polysaccharide biosynthesis in	Morona, J.K., Morona, R. and Paton, J.C.	1 (bases 1 to 5832)	Streptococcus.	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;	Streptococcus pneumoniae	Streptococcus pneumoniae.		AF105113.1 GI:4406246	AF105113	(aliA) gene, partial cds:	dTDP-L-rhamnose synthase (cps19AO) genes, complete cds; and AliA	(cps19AM), dTDP-glucose-4,6-dehydratase (cps19AN), and	transferase (cps19AL), dTDP-4-keto-6-deoxyglucose-3,5-epimerase	glucosamine-2-epimerase (cps19AK), glucose-1-phosphate thymidylyl	unit transporter (cps19AJ) gene, partial cds; UDP-N-acetyl	Streptococcus pneumoniae type 19A putative oligosaccharide repeat	AF105113 5832 bp DNA BCT 09-SEP-1999		

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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Submitted (10-NOV-1998) Molecular Microbiology Unit, Women's
Children's Hospital, 72 King William Rd, Adelaide, SA 5006,
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ALIIGDNIYHGPGLSTMLQKAAKKEKGATVFGYQVKDPERFGVVEFDTDMNAISIEEK
PEYPRSNYAYTGLYFYDNDVVEIAKQIKPSARGELEITDVNKAYLNRGDLSVELMGRG
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ALVMLISMGVTLVTTYLLNSLELTVVSIVVLLALRSIIAELILSKKLDVSVKKDIVLE
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AALAAFYLGIKVGHVEAGLRTYNLOSPFPEEFNROSTSIIATYHFAPTELAKENLLKE
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                                                                                                                                                                                                  EYGRYLLRLIGEA"
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transporter"
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AF094575 18754 bp DNA BCT 09-SEP-1999 Streptococcus pneumoniae serotype 19A DexB (dexB) gene, partial sequence; capsular polysaccharide biosynthesis operon, complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease AliA (aliA) gene, partial complete sequence; and oligopeptide permease alia (aliA) gene, partial complete sequence; and oligopeptide permease alia (aliA) gene, partial complete sequence; and oligopeptide permease alia (aliA) gene, partial complete sequence; and oligopeptide permease alia (aliA) gene, partial complete sequence alia (aliA) gene, partial alia (aliA) gene, partial alia (aliA) gene, partial alia (aliA) gene, partial alia (alia (alia (aliA)) gene, partial alia (alia (alia (alia (ali
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GEGKNVRDWIHTNDHSSGVWTILTKGQIGETYLIGADGEKNNKEVLELILKEMGQPAD
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/db_xref="GI:4406250"
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Direct Submission
Submitted (23-SEP-1998) Microbial Microbiology Unit, Women's a Submitted (Baselian Ref. North Adelaide, SA 5006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morona, J.K., Morona, R. and Paton, J.C.
Comparative genetics of capsular polysaccharide biosynthesis
Streptococcus pneumoniae types belonging to serogroup 19
J. Bacteriol. 181 (17), 5355-5364 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Australia
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Analysis of the 5' portion of the type 19A capsule locus identifies
two classes of cpsC, cpsD, and cpsE genes in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae Bacteria; Firmicutes; Bacillus/Clostridium
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AF094575.1 GI:3907597
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                                                                                                                                                                                                GNNQKDKLTHAGIYGVDSSIHTLENLYGVDINYYVRLNETSFLKLIDLLGGVDYYNDQ
DFTSLHGKFHFPVGNVHLDSEQALGFVRERYSLADGDHDRGRNQQKVIAAILQKLTSS
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RYLNIVPALVLLVALVGLLLIIYKKAEKFTIFLLVFSILVSSVSLFAVQQFVGLTNR
LNATSNYSEYSISVAVLADSEIENVYQLMSVTAPTGTDNENIQKLLADIKSSQNTDLT
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                                                                                                                                                                                                                                                                           KTSKDQSFNIYVSGIDTYGPISSVSRSYVNILMTVNRDTKKILLTTTPRDAYVPIADG
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                                                                                                                                                                           AMPDSNLYMMEINDSSLASVKTAIQDVLEGR*
                                                                                                                                                                                                                                                                                                  VNOSSSYLAAYKSLIAGETKAIVLNSVFENIIESEHPDYASKIKKIYTKGFTKKVEAP
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/protein_id="AAC78662.1"
/db_xref="GI:3907598"
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/db_xref="taxon:1313"
                                                                                                                          'gene="cps19aB"
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1733 3178
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|733. .3178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYFYFYISDYGRNFFKRGYLIELVQTLKYILFFALAISISNFFLEDRFSISRRGMIYF
LLLHYFLVYVLNPFIKWYWKRAYPNFKGSKKILLLTAMSRVEKYLDRLIESDDYVGEL
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LVSIVLPLIRKDGGSAFFAQTRIGKNGRHFTFYKFRSNCVDAEEKKRELMEQNTMQG
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7475. .8257
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7475. .8257
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SQGLCDTNIENLFVIQAGSVSPNPTALLQSKNFTTMLETLRKYFDYIVVDTAPVGVVI
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QVNSSHVLKSKLEGERYKFMKKRAQYFLERDLVHIIASDMHNVDSRPPHMAEAYDLVS
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DWPAKTLTSKVQVTVPADTRIVSISVKDKQPEEASRIANSLREVAAEKIIAVTRVSDV
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'transl_table=11
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'function="chain
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protein_id="AAC78665.1"
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'function="chain
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Best Local :
                                                                                                                                                                                                                                                                 13888 CGTGGTTTTGCCTGGTTGGATACGGGA 13914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                             ATTACAGACGTTAACAAGGCTTACCTAAATCGTGGTGACCTTTCTGTTGAGCTGATGGGG 13887
                                                                                                                                                                                                                                                                                                                                                                                                      attactgacgacaaagaccccgaccgagatggtcggggtctttttgttgtggtgctgtga 91
                                                                                                                                                                                                                                                                                                               cgtgttgtccaaccgtattattccgga 118
                         HTG;
                                                                                                                       Homo sapiens chromosome
                                           AC024405.6 GI:15148297
                                                                                                                                              AC024405
                                                                                           IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.0%;
nilarity 59.8%;
Conservative
                      HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKLQELYESDSEIDVLINHENAGFARGNNVAYQFAKEKYKPDFMVIMNNDIEIETEEF
EKIVTDIYRKEKFHLLGPDIFSTTYQLHQNPKRLTHYTYEEVKALNEKFKKGSQVSLA
LKIKCWLKSSKVLRTAIYQNRRKKKSVDYRKQVENPILHGSFIVYSRDLIEKEEYAFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transiation="wtylfllclttfltltfeyffafnodliappvvmsvmflissvfa
Linvommifysglaylliisgiivfsmfllalingpsltmytstydrlidioffwkial
Tiivolliilyarreinnlalishgyfosnfomffryeggelfvrystrildioff
Vsayifgytfinnffiyshkrskdllllvpflifisktllsggrldiikiliayvvma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPREGYDKLPGIFKDRIIAGKYQVLAYQYCDTLHCYFPRLFLLEDERKRLGLPRNTNL
GLHLIDIIPLDGAPNHSFLRKLYFGKVYMYRFLASLGTTYVGDHVDMHSAKQKLIIGF
FKKLGFAKLFPQNYVLRRLDNLYKKYDMKKQKYAGTINASLFAKEVMPVEIWGEGVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="cps19aJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSIEQYSFTTISLFTLVFIVLVYLMAFFYWNLDFHRGKLVIKLSDTSIKSEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIQQKRKYGWDKVISHKYMRLGFVGLIAGIPTFYYSLFLSGRSTTRTVFESISTYLGG
SIQHFNQYIQNPIGVAEVFGDESFVAIMNILGNLGFVNYNSTVHLEFRQLGITMGNVY
FFFRRPWHDFGLVGMYIFSFVVGVFFAIFYLKLRKSRAGFKLDIHTIIYSYFFYWIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="polysaccharide polymerase Cps19a1"
/protein_id="AAC78671.1"
/db_xref="GI:3907607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNTFFYYETEILDYEAELKGYKRIYTPKIKVLHHQNVATNQVYTNLVEKTLFSNKCNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="cps19aJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"putative rhamnosyl transferase Cps19aH"
/protein_id-"AAC78670.1"
/db_xref-"G1:3907606"
/translation-"MFCYIILHYKVLEETISCVKSIKEGNSNTKQIVIIDNESNNGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFEDAFFKVPTEYDRYLKRLYGENYLHEEPSDDEKKSHLGGQ'
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/protein_id="AAC78669.1"
/db_xref="GI:3907605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="cps19aI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="cps19aH"
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                                                                                                                                            174118 bp
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Pred. No.
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clone RP11-574M7
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                                                                                                                     SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
25 ttcgagcattactgacgacaaagaccccgaccgagatggtcggggtcttttttgttgtggt 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
Lileu,C., Lil,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrin,J.,
Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Morman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trigilio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B.,
Mu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 11, 2001 this sequence version replaced gi:15144553. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Höwland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E.,
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1 (bases 1 to 174118)
Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-574M7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                            54806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by the finished sequence as soon as it is available and the accession number will be preserved.

1 174118: contig of 174118 bp in length.
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Center clone name: 574_M_7
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                              Conservative
                                                                                                                                                                                                                                                                      /clone="RP11-574M7"
/clone_lib="RPCI-11
34652 c 31384 g
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="11"
                                                                                                                        22.9%;
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                                                                                                                           Score 29.6;
Pred. No. 53;
                                                                                              Mismatches
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53276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 185341)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
On Dec 18, 2000 this sequence version replaced gi:11693354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 185341)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel.N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC069403.11 GI:11878497
                                                                                                                                                                                                                                                                                                          Insert size: 113180; agarose-fp
Insert size: 185241; sum-of-contigs
Quality coverage: 15.2x in Q20 bases; agarose-fp
Quality coverage: 9.3x in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                              as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990319
Consensus quality: 184714 bases at least Q40
Consensus quality: 184960 bases at least Q30
Consensus quality: 185096 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Stanford DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Vector: M13mp18; X02513; 100% of resequencing Vector: plasmid; plasmid-accession; Chemistry: Dye-primer; 1% of reads Chemistry: Dye-terminator Big Dye; 99% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: 932
Center clone name: RP11-54B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://sequence-www.stanford.edu/group/human/Contact: hum-info@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: SDSTDC
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- Project Information
                                                        .185341
                                                                                                   43623: contig of 43623 bp in length 43723: gap of unknown length 185341: contig of 141618 bp in length

    Summary Statistics

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                                                                              Qualifiers
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                                                                                                      in length
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WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of reads
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KEYWORDS
SOURCE
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AL162413/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71459 TTGGTCCAGTCCTGACCAGTCTTATCCAGATCTGCATGGTCTTGTCCAGTTTGGTCTGGT 71518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71519 CCTGTCCAGTCCTGTCCAGTCTTA 71542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 ttcgagcattactgacgacaaagaccccgaccgagatggtcggggtctttttgttgttgt 84
                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L0875; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 326784 bases at least Q40
Consensus quality: 328297 bases at least Q30
Consensus quality: 328297 bases at least Q20
Consensus quality: 329246 bases at least Q20
Insert size: 330109; sum-of-contigs
Insert size: 330557; 19.2% error; agarose-fp
Consensus quality: 328297 bases; sum-of-contigs Quality
Coverage: 6.30x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA109M17
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced g1:15029110
                     * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                               coverage: 7.15x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corby, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58857
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clone_end:SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ***, 11 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43724.
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1: .43623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34339 c
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59586: contig of 59586 bp in length
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Pred. No. 53;
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12-AUG-2001 WORKING DRAFT

Louis,

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RESULT
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                                                                                                                                                                                                                                                                                                     BASE COUNT
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Best Local
                                                                                                                                                                                                  Matches
                                                          174007
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                                                                                     85 gctgtgacgtgttgtccaaccgta 108
                                                                                                                                              25 ttcgagcattactgacgacaaagaccccgaccgagatggtcggggtctttttgttgtggt 84
                                                        CCTGTCCAGTCCTGTCCAGTCTTA 173984
                                                                                                                           TTGGTCCAGTCCTGACCAGTCTTATCCAGATCTGCATGGTCTTGTCCAGTTTGGTCTGGT 174008
                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:04963"
64007 c 60342 g 100117 t 1
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/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment:03601"
                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:03292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment:00694
ragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_fragment:03747 ragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="assembly_fragment:04814
ragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment:03121
ragment_chain:2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:01096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11.1"
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288703: contig of 6390 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of 331109: cc.
                                                                                                                                                                                                                                                                                                                                                                                                                        e="assembly_fragment:01842"
                                                                                                                                                                                                                 22.9%;
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22077: contig of 2985
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58058: contig of 98372 bp in length
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contig of 20972 k
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                                                                                                                                                                                                                 Score 29.6;
Pred. No. 54;
                                                                                                                                                                                               Mismatches
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                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston,R.H.
Direct Submission
Submitted (14-JUN-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Aug 12, 2001 this sequence version replaced gi:14423621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye; 99% of Assembly program: Phrap: version 0.990319
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179759)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC092021 179759 bp DNA HTG HOMO Sapiens chromosome UNK clone RP11-420H12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0420H12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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10101
11204
/note="assembly_name:Contig15"
                                                      10101. .11203
                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                  'note="assembly_name:Contigl4"
                                                                   note-"assembly_name:Contigl"
                                                                                                      clone="RP11-420H12"
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10100: gap of unknown length
11203: contig of 1103 bp in length
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                                                                                                                      Chemistry: Dye-primer ET; % of reads (hemistry: Dye-terminator Big Dye; % of reads (hemistry: Dye-terminator Big Dye; % of reads Assembly program: Phrap; version 0.990319 (consensus quality: 180703 bases at least Q30 (consensus quality: 184821 bases at least Q30 (consensus quality: 186902 bases at least Q20 (consensus quality: 186902 bases quality: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                     Insert size: 203000; agarose-fp
Insert size: 189919; sum-of-contigs
                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; % Sequencing vector: plasmid; %
                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_NH0343F24
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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178628. .179759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001 this sequence version replaced gi:14196415
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   4.39 in Q20 bases;
4.73 in Q20 bases;
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Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Information
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sum-of-contigs
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ORIGIN
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                                                                                                                                                                                                     51253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is, a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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18163
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42453 c 43073 g 53129 t
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171236. .190919
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163084. .166817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="UNK"
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50980. .152042
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11956. .74275
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                                                                                                                           Score 29.4; DB Pred. No. 62;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L00752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 202171 bases at least Q40 Consensus quality: 202224 bases at least Q30 Consensus quality: 202224 bases at least Q20
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PROGRESS ***, in ordered pic
AL356219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 202224; sum-of-contigs
Insert size: 181975; 8.7% error; agarose-fp
Quality coverage: 10.85x in Q20 bases; sum-c
coverage: 12.20x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                  Similarity 60.8
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA430C15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced
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39332 c 40682 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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Pred. No. 62;
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AUTHORS
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SOURCE
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Marphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigllio, J.,
Vonstilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Talama, P., Ve, N.,
Vonno, G., Talama, P., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Talama, P., Ve, N.,
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Vonno, G., Talama, P., Talama, P., Ve, N.,
Vonno, G., Talama, P., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Talama, P., Ve, N.,
Vonno, G., Talama, P., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Ve, N., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Ve, R., Vela, R., Vonno, A., Talama, P., Ye, W.J.,
Vonno, G., Talama, P., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Vela, R., Vonno, A., Talama, P., Ye, W.J.,
Vonno, G., Talama, P., Ye, W.J.,
Vonno, G., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Walson, B., Wu, X., Wyman, D., Ye, W.J.,
Vonno, G., Talama, P., Vela, R., Vonno, A., Talama, P., Ye, W.J.,
Vonno, G., Talama, P., Vela, R., Vonno, A., Talama, P., Ye, W.J.,
Vonno, G., Talama, P., Walson, B., Wu, Y., Wyman, D., Ye, W.J.,
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Vonno,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                            IN PROGRESS ***, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 6904: contig of 6904 bp in length 6905 7004: gap of 100 bp 7005 24083: contig of 17079 bp in length 24084 24183: gap of 100 kp
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Center clone name: 5_0_16
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                                                                                                                                199325 199424: gap of 100 1
199425 203674: contig of 4250
                                                                                                                                                                                                                                                                                                                                         24184 24183: gap of 100 bp
24184 74907: contig of 50724 bp in length
74908 75007: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24084 24183:
24184 7490
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                                                                Location/Qualifiers
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 227470 bases at least Q30
Consensus quality: 228935 bases at least Q20
Consensus quality: 228935 bases at least Q20
                                                                                                                                                                                                                                                                                 Insert size: 229738; sum-of-contigs
Insert size: 212606; 9.8% error; agarose-fp
Quality coverage: 8.27x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Sanger Centre
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 26, 2001 this sequence version replaced gi:15021038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL591946 230838 bp DNA HTG. Mus musculus chromosome 15 clone RP23-290M7, PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                  coverage: 9.20x in Q20 bases; agarose-fp
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Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence
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/clone_lib="RPCI-23"
1. .20354
                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="15"
                                      /clone-"RP23-290M7"
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46593 c 44067 g 52872 t 405 ot
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Pred. No. 62;
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                                   2 (bases 1 to 1877)
Jang, J.S., Hahn, Y., Park, C.
Direct Submission
                                                                                                    1 (bases 1 to 1877)
Jang, J.S., Hahn, Y., Park, C. and Chung, J.H.
Identification of an evolutionary conserved mitochondrial carrier family from various organisms
Submitted (06-AUG-1999) Department of Biological Sciences, Korea Advanced Institute of Science and Technology, 373-1 Gusong-dong
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                     Western European house mouse.
Mus musculus domesticus
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2 (bases I to 1928)

2 (bases I to 1928)

Jang,J.S., Hahn,Y., Park,C. and Chung,J.H.

Direct Submission

Submitted (06-CCT-1999) Department of Biological Sciences, Korea

Submitted (06-CCT-1999) Department of Biological Sciences, Korea

Submitted (06-CCT-1999) Topic and Technology, 373-1 Gusong-dong
Advanced Institute of Science and Technology, 373 Yusong-gu, Taejon 305-701, South Korea 3 (bases 1 to 1928)
Lee, J., Hahhr, Y. and Chung, J.H.
Direct Submission
Submitted (26-NOV-1999) Department of Biological
                                                                                                                                                                                                                                                                                                                                                                                                                               AF192558 1928 bp mRNA ROD 26-NOV-1999 Mus musculus domesticus mitochondrial carrier homolog 1 isoform b (Mtchl) mRNA, complete cds; nuclear gene for mitochondrial product.
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Jang, J.S., Hahn, Y., Park, C. and Chung, J.H.
Evolutionarily conserved mitochondrial car.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDVVFLMGCNLLAHF
INAYLVDDSFSQALAIRSYTKFVMGIAVSMLTYPFLLVGDLMAVNNCGLRAGLPPYSP
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/sub_species="domesticus"
/db_xref="taxon:10092"
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                                                              Krol, J.E. and Skorupska, A.M.
Direct Submission
Submitted (29-DEC-1995) Jaroslaw E.
                                                                                                                                          l (bases 1 to 2193)

Krol,J. and Skorupska,A.

Identification of genes in Rhizobium leguminosarum bv. trifolii
whose products are homologues to a family of ATP-binding proteins
Microbiology 143 (Pt 4), 1389–1394 (1997)
                                                  M.Curie-Sklodowska
                  Cloned on
                                                                                                                                                                                                                                                           Rhizobium leguminosarum bv. trifolii.
Rhizobium leguminosarum bv. trifolii
                                                                                                                                                                                                                                                                                                              U44387.1
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On Nov 26, 1999 this sequence version replaced
Location/Qualifiers
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                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
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ed on cosmid pARF136 complementing Exo-mutations, Blochim. Pol. 38, 423-435 (1991).
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1918
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PAHRAHPRHPRPAAQPSARRWDGGPGAPGSGDNAPTTEALFVALGAGVTALSHPLLYV
KLLIQVGHEPMPPTLGTNVLGRKVLYLPSFFTYAKYIVQVDGKIGLFRGLSPRLMSNA
                                                                                                                                                                                                                                                                                                              GI:1172153
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/sub_species="domesticus"
/db_xref="taxon:10092"
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/db_xref="GI:6468760"
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               Skorupska, A.
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                                                                                                                                                                              Rhizobium leguminosarum
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                              ORF3 gene; prsD gene; prsE gene
Rhizobium leguminosarum
                                                                                                                                                                                                                                                                                                              Rhizobium leguminosarum

x98117

x98117.1 GI:1806273
Krol.J. and Skorupska,A.
Identification of genes in Rhizobium leguminosarum bv. trifolii
whose products are homologues to a family of ATP-binding proteins
                                                                                                                                                       Rhizobiaceae; Rhizobium.
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GEGVIVVDPRCONIOHLTGGIVEELLVSENDHVTAGQVLIRLDGTTRANLSIVESTL
AQLYAARARLKAERIGAESFEVEENITDLTSSTSAQKL"
1 596 c 684 g 485 t
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aeruginosa aprE gene, GenBank Accession Number X64558 and
to product encoded by Erwinia chrysanthemi prtE gene,
GenBank Accession Number M60395"
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SUVGNGYATLSKIFRIALQSGTLATGAILVIQGQASSGIIIAGSILTSRALAFVEAAI
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to product encoded by Erwinia chrysanthemi prtD gene,
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/db_xref="GI:1172154"
/translation="MQGGLVEIGIASALINILYLTSSPFMLEVYDRVIPSKSIPSLAV
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/db_xref="GI:1172155"
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SEGLRAGSALGVIGYSASGKSSLARAMMGIWPTVRGSIRLDGAALDQWDGDALGRHI
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.RDFDQIRTFLSGMGPTAMEDLPWLPFYIVICFLFHPAIGYIAIGGSLVLAILTFMTN
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/strain="TAl"
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Pred. No. 62;
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29, 1997 this sequence version replaced
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/translation="macrotrap"
/translation="
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/db_xref="GI:1806274"
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RSISCTVSTSRAADRTSSRAFVHTVNGVIDPGQTLMLVVPENNELTVEAKVATRDIDQ
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/protein_id="CAA66800.1"
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/sub_species="trifolii"
/strain="TA1"
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/protein_id="CAA66799:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
2 (bases 1 to 21984)
Jang, J.S., Hahn, Y., L
Direct Submission
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52; Conserv
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/standard_name="AT_rich"
/note="Low_complexity"
complement(1484. .1598)
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/standard_name="ORR1C"
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/note="SINE"
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                                                                                                                                                            /rpt_unit-ttta
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/note="Low_complexity"
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Query Match
Best Local Similarity
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Search completed: March 28, 2002, 15:20:21 Job time: 8185 sec

Дb

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sult No. Score 1 28.4 2 27.6 3 27.6	% Query Match 22.0 21.4 21.4	Query Hatch Length DB 22.0 936 18 21.4 366 18 21.4 366 18 21.4 366 18	DB 18 18	SUMMARIES ID AAT79329 AAT67819 AAT77499	Description DNA encoding Archa H. pylori cell env H. pylori inner me
1 28.4		936	18	AAT79329	DNA enc
2 27.6		366	18	AAT67819	H. pvl
3 27.6		366	18	AAT77499	H DV
4 27.6		1422	20	AAX35720	CDWA SH
5 27.6		1613	20	AAX35721	CDNA OF
6 27.6		2090	19	AAV68588	Nincleo+1de compa
7 27.6		2090	19	AAV38564	Human
8 27.6		2150	22	AAH81781	Himan differential
9 27.6		26778	21	AAA81477	N HOD
10 27.6		349980	21	AAF21612	Neisseria moningit
11 27.4		1356	22	AAS21265	Human cDNA sequenc

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19.7	19.7	19.7	19.7	19.8	19.8	19.8	20.0	20.0	20.2	20.2	20.2	20.2	20.2	20.2	20.3	20.3	20.3	20.3	20.3	20.3	20.3	20.3										21.2	
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21																								•									
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ALIGNMENTS

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RESULT
AAT79329
21-AUG-1997.
                  WO9730160-A1.
                                                                                                                              CDS
                                                                                                                                                                                                     Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss.
                                                                                                                                                                                   Archaeoglobus fulgidus strain VC16.
                                                                                                                                                                      Key
                                                                                                                                                                                                                                             DNA encoding Archaeoglobus fulgidus esterase VC16-16MC
                                                                                                                                                                                                                                                                                                          AAT79329 standard; DNA; 936 BP
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559.561, aa:Ile)
691.693, aa:Asn)
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RESULT
AAT67819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAW23076) of Archaeoglobus fulgidus VC16, an isolate that grows optimally at 85 deg C and pH 7.0. It can be amplified from a pBluescript vector by PCR (see AAT79317-18). Claimed, newly identified polynucleotides (AAT79321-30) encoding esterases (AAW23069-77, AAW23088) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes can'd to an alpha-keto acid using a claimed esterase. The enzymes can'd salso be useful as ripening starters in cheese making, in lighin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lighocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Reid J, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 50-51; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-425035/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1997;
                                                                              Cytoplasmic; vaccine; prevention; treatment; identification; binding compound; bacterium; bacteria; inhibitor; duodenal ulcer disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 936 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA sequence codes for thermostable esterase VC16-16MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      paper manufacture, and to study plant resistance to disease
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Кеу
                               Helicobacter pylori
                                                             diagnosis; ds.
                                                                                                                                            H. pylori cell envelope inner membrane protein ORF 486075.aa
                                                                                                                                                                            04-AUG-1997
                                                                                                                                                                                                           AAT67819
                                                                                                                                                                                                                                             AAT67819 standard; DNA; 366
                                                                                                                                                                                                                                                                                                                           778
                                                                                                                                                                                                                                                                                                                                                                                         718
                                                                                                                                                                                                                                                                                                                                            62 ggtcggggtctttttgttgtggtgctgtgacgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 56.4
53; Conservative
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                                                                                                                                                                             (first entry)
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 Location/Qualifiers
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Pred. No. 2.9;
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                                                                                infection; envelope;
life cycle; activator;
chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                     AAT77499
                                                  RESULT
                                                                                                                                                                                                                                                                              This sequence encodes a Helicobacter pylori cell envelope protein that may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, consequence of the pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino carid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide C isolated from H. pylori by PCR amplification for recombinant polypeptide C Note: This DNA sequence is not reproduced in the specification and case when derived from the related specification, W09719098.
                                                                                                                                                                                             Matches
                                                                                                                                                                                                        Query Match
Best Local
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berglindh OT,
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                                                                                                                                                                                                                                                           Sequence 366 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page -; 1481pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW20524.
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AAT77499;
                        AAT77499 standard; DNA; 366
                                                                                      153 ggtggttgtagcgagtgctatc
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les 48; Conser
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                                                                                                      tgtggtgctgtgacgtgttgtc 100
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95US-0487032
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                                                                                                                                                                                                                                                           109 A; 62 C; 79 G; 109 T; 7 other;
                                                                                                                                                                                                         21.4%;
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                           ВP
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                                                                                                                                                                                                                     Score 27.6;
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316
316
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                                                                                                                                                                                                                        DB 18;
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                                                                                                                                                                                                                       Length 366;
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11-AUG-1997

(first entry)

0

H. pylori inner membrane protein ORF 486075.aa

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are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are 20 also useful for generating vaccines for immunising subjects against H. 21 color or for use in detecting the presence of Helicobacter species in 22 a sample. Antisense nucleic acid sequences of these sequences are 23 cused to inhibit expression of a gene from Helicobacter species. H. 26 cused to inhibit expression of a gene from Helicobacter species. H. 27 cused to inhibit expression of a gene from Helicobacter species. H. 27 cused to inhibit expression of a gene from Helicobacter species. H. 27 cused to inhibit expression of a gene from Helicobacter species. H. 27 cused to inhibit expression of a gene from Helicobacter species. H. 27 cused to inhibit expression of a gene from Helicobacter species. H. 28 cused to inhibit expression of a gene from Helicobacter species. H. 28 cused to inhibit expression of a gene from Helicobacter species. H. 28 cused to inhibit expression of a gene from Helicobacter species. H. 28 cused to inhibit expression of a gene from Helicobacter species. H. 28 cused to inhibit expression of a gene from Helicobacter species. H. 29 cused to inhibit expression of a gene from Helicobacter species. H. 20 cused to inhibit expression of the section of 
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Best Local Similarity
                                                                                             Matches
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Note: The ORF/protein r

from the related speci/
                                                                                                                                                                                                  Sequence 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes a Helicobacter pylori inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori nucleic acid sequences and related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-298052/27.
P-PSDB; AAW24680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1996;
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                        93
gatcgctttgatcattgaaaaagacaaggtctatgagcaagtgggatcggtgcgttttgt 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for diagnostics and therapeutics
                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 122;
                                                                                           Conservative
                                                                                                                                                                                                  BP;
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                                                                                                                                                                                             109 A; 62 C;
                                                                                                                                                                                                                                     otein reference number for this sequence was obtained specification, W09640893.
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                                                                                                             21.4%; 58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori inner membrane protein.
been strongly linked to chronic gastritis and
The nucleic acid sequences of the invention
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                                                                                         0;
                                                                                       Score 27.6; I
Pred. No. 4;
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(pos: 301.
(pos: 304.
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(pos: 355.
(pos: 361.
                                                                                                                              DB
                                                                                                                              18;
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GGTTGTCAATGATATTCTGTAGTCGAGTGTTCTCCTGTTTTATTGTTTCACATT TCTGCTGCAATTCATTTCATGATTTATTCGCTCAATGTCTGCGAGCTGAGTACTTCT

67

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Query Match Best Local Matches

l Similarity 60; Conserv

Conservative

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Mismatches

54;

Indels Length

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21.4%; 52.6%;

Score 27.6; Pred. No. 6

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RESULT 4
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                   AAX35694-X35747 represent cDNA sequences that encode novel polypeptides (AAY02358-84) which are identified from a human placental cDNA library by the signal sequence trap (SST) method. The polypeptides have a broad range of physiological activity, including immunisation against and inhibition of infections, allergies and cancer; regulation of tissue formation and repair; activin/inhibin activity; Chemokine/Cytokine activity; blood coagulation regulation; and receptor/ligand agonist or antagonist activity. The polypeptides can be used for prevention and treatment of disorders including infections by bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and hormonal disorders; inmune disorders (including severe combined immunodeficiency (SCID) and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
Sequence 1422 BP; 538 A; 213 C;
                                                                                                                                                                                                                                      Claim 5;
                                                                                                                                                                                                                                                                    Polypeptides identified human cDNA library
                                                                                                                                                                                                                                                                                                                                WPI; 1999-277254/23
                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine activity; blood coagulation regulation; agonist; antagonist; metabolic disorder; hormonal disorder; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection; allergy; cancer; regulation; tissue formatic activin activity; inhibin activity; chemokine activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding a protein identified by the signal sequence trap method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    severe combined
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                                                                                                                                                                                                                                     139-140;
                                                                                                                                                                                                                                                                                                                                                             Shibayama
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immunodeficiency; SCID; AIDS; thrombosis; cancer;
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332 G;
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339 T;
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0 other;
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AAX35721/c
ID AAX35721 standard; cDNA; 1613
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Best Local
                                                                                                                                                                                                                             AAX35694-X35747 represent cDNA sequences that encode novel polypeptides (AAY02338-84) which are identified from a human placental cDNA library by the signal sequence trap (SST) method The polypeptides have a broad range of physiological activity, including immunisation against and inhibition of infections, allergies and cancer; regulation of tissue formation and repair; activiny/inhibin activity; chemokine/cytokine activity; blood coagulation regulation; and receptor/ligand agonist or antagonist activity. The polypeptides can be used for prevention and treatment of disorders including infections by bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and hormonal disorders; immune disorders (including severe combined immunodeficiency (SCID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; allergy; cancer; regulation; tissue formation; tissue repa
activin activity; inhibin activity; chemokine activity;
cytokine activity; blood coagulation regulation; agonist; antagonist;
metabolic disorder; hormonal disorder; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides identified by the signal sequence trap method from human cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-277254/23.
P-PSDB; AAY02371.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 141-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukushima D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a protein identified by the signal sequence trap method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX35721;
                                                                                                                                                                                     Sequence 1613 BP; 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ONOY ) ONO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09918126-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
 669
                                                         729
                            67
                                                      gggtctttttgttgttgtgctgtgacgtgttgtccaaccgtattattccggact 120
GGTTGTCAATGATATTCTGTAGTCGAGTGTTCTCCTGTTTTATTGTTTCACATT 616
                                                                                                                 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence trap method; SST method; immunisation;
                                                                                                                             Similarity
                                                                                                                                                                                                                    thrombosis;
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0274674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP04514.
                                                                                                                             21.4%;
                                                                                                                                                                                       Α,
                                                                                                                                                                                                                  cancer; and traumatic or surgical
                                                                                                                                                                                                                                                                                                                                                                                                      281pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ß
                                                                                                                                                                                     243 C;
                                                                                                                Score 27.6; DB Pred. No. 6.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tada
                                                                                                                                                                                       359 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ħ;
                                                                                                                                                                                     387 T; 0 other;
                                                                                                                                            DB
                                                                                                                54;
                                                                                                                                            20;
                                                                                                                                            Length
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibition;
                                                                                                                                                                                                                    wounds
                                                                                                                                            1613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue repair;
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                                                                                                                Gaps
                                                         670
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AAV68588/c RESULT

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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of a human nuclear protein (HEC) used in the method of the invention to diagnose cell growth abnormalities. Fragments of HEC are used to detect HEC-encoding nucleic acid, in usual hybridisation or amplification assays, while antibodies are used in conventional immunoassays to detect HEC or peptides. HEC is used to modulate cell cycle progression (by disrupting chromatid separation) and antibodies are used to disorder sister chromatid alignment and separation in interphase cells, disrupting mitosis, particularly for control of malignancy and other cell growth abnormalities at the mitosis stage. Antibodies can also be used for protein purification, to
                                                                                                              1239
1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding human highly expressed in cancer nuclear protein - used for diagnosis and for modulation of the cell cycle control malignant and other cell growth abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolate sequences encoding HEC or related proteins; to study HEC distribution in cells and to isolate antigens by immunoprecipita HEC may also be used in vaccines and antibodies for passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 55-58; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allred DC,
Osborne CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence encoding the human nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 2090 BP; 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplification; antibody; immunoassay; malignancy; mitosis; antigen;
immunoprecipitation; immunisation; vaccine; ss.
                                                  67 gggtctttttgttgtggtgctgtgacgtgttgtccaaccgtattattccggact 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-594481/50
GGTTGTCAATGATATTCTGTAGTCGAGTGTTCTCCTGTTTTATTGTTTCACATT
                                                                                                              TCTGCTGCAATTCATTTCTTTCATGATTTATTCGCTCAATGTCTGCAACTGAGTACTTCT 1180
                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chamness
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "human nuclear protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                       21.4%;
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                                                                                                                                                                                                                                                                                                                                                                      A; 362
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                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                       Score 27.6;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                      C;
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                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      514 T; 0
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                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                            other
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                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                        2090;
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                                                                                                                                                    Coloned from a human B cell cDNA library by its interaction with the Co-terminus of Rb in a yeast two-hybrid system. This fragment was used as a probe to screen a human B cell cDNA library, and the Colonest clone obtained included the full-length coding sequence for HEC. HEC nucleic acid segments and their encoded polypeptides are important in modulating mitosis and thus regulating cell modulating mitosis and thus regulating cell modulating mitosis and thus regulating cell malignancies and other cell growth abnormalities at the cell mitosis stage. DNA segments encoding HEC are also useful to produce HEC protein/peptides and to detect HEC-encoding sequences (e.g. from related species), by contacting with a nucleic acid sample under suitable conditions and detecting hybridisation (claimed kits are provided). HEC peptides are useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XZ
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ID AAV38564 standard; cDNA; 2090 BP
                                                                        Matches
                                                                                        Query Match
Best Local
1239 TCTGCTGCAATTCATTTCTTTCATGATTTATTCGCTCAATGTCTGCAACTGAGTACTTCT 1180
                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA clone codes for a novel human nuclear protein (see AAW62596) designated HEC (highly expressed in cancer) that appears to be crucial for normal mitosis, possibly in regulation of normal progression of M phase. A 1.8 kb cDNA fragment was originally
                                                                                                                                                 Sequence 2090 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 59-62; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human nuclear protein HEC modulating mitosis useful to, e.g control cell malignancies and other cell growth abnormalities at mitosis stage and to produce HEC protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW62596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitosis; cell cycle; cell proliferation; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEC gene; highly expressed in cancer; human; nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nuclear protein HEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV38564;
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                                                                                     Local
                   7 tetgetegtagegattaettegageattaetgaegaeaaagaeeeeggaeegagatggteg 66
                                                                                                                                                                           may be administered to cells to disrupt chrom so modulate cell cycle progression (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-377401/32
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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2070..2075
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                                                                                                                                                750 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·Lee W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                   21.4%;
                                                                                                                                                362 C;
                                                                 Score 27.6; DB: Pred. No. 6.9; 0; Mismatches
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                                                                                                                                              464 G;
                                                                                                                                                                                        disrupt chromatid separation
                                                                                                                                                514 T; 0
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                                                                   54;
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                                                                                                                                                other;
                                                                 Indels
                                                                                              Length
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TCTGCTGCAATTCATTTCTTTCATGATTTATTCGCTCAATGTCTGCAACTGAGTACTTCT 1180

999tctttttgttgtggtgctgtgacgtgttgtccaaccgtattattccggact 120

GGTTGTCAATGATATTCTGTAGTCGAGTGTTCTCCTGTTTTATTGTTTCACATT

Matches Query Match Best Local

60;

Conservative

0;

Mismatches

54; 22;

Indels Length 2150;

0;

Gaps

0;

66

Local Similarity

21.4%;

Score 27.6; Pred. No. 7;

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                                        modulating expression of (I) (by gene therapy, antisense RNA or ribozy methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes the are not primary targets for tumour initiating mutations). AAH81492-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
          Sequence
                                                                                                                                                                                                                       effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
                                                                                                                                                                                                                                                                                suppressor genes. (I), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the
                                                                                                                                                                                                                                                                                                                                This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 444-445; 579pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483415/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenthal A, Hinzmann B, Schaefer R, Zu
Grips M, Hellriegel M, Schmitz A, Sers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (META-) METAGEN GES GENOMFORSCHUNG MBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differential transcription; human; rat; tumour cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ras modulator; Class II tumour suppressor gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2150 BP; 810 A; 362 C; 464 G; 514 T; 0 other;
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ers C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell; cytostatic;
gene therapy; ss
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                                                                                                                     genes that
                                                                                                                                                                                                             ribozyme
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RESULT
AAA81477/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have failed mainly due to antigen tolerance sequences may provide an opportunity. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N. meningitidis partial DNA sequence gnm_25 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 the AAA81259 and AAA81301 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA81477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA81477 standard; DNA; 26778 BP
Sequence 26778 BP; 6602 A; 7008 C; 6846 G;
                                                                                                                                                                                                                                                                                                              AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibot against them, can be used in the manufacture of a composition. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 524-531; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-318079/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frazer CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200022430-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; vaccine;
Meningococcus B; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; Neisseria gonorrheae; genome;
                                      other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hickey E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galeotti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0103794
99US-0132068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US23573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; diagnosis; infection; antibacterial;
MenB; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson
. C, Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terson J,
Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tettelin H,
Ratti G, S
    6318 T; 4 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenic;
identification;
                                                                                                                                                                                                                                                                                                                                    and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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Matches Query Match

Local Similarity

21.4%;

Conservative

0, Score Pred.

Mismatches 27.6; No. 15

Indels Length 26778;

0;

Gaps

0;

Sequence 349980 BP; 86473 A; 95646 C;

85908 G;

81953 T;

0 other;

DВ

21; 29;

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RESULT 10
AAF21612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID XXX ACC XXX
The present invention describes the full length genome of CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 cc to AAF21613 represent fragments of the NMB genomic sequence, as the CC sequence was too long to go in a record on its own it was split into 8 cc sequences which overlap each other at the beginning and end of each CC sequence by 4980 bp (i.e. the last 49980 bp of AAF21544 is repeated at CC the beginning of AAF21607, the last 49980 bp of AAF21547 are repeated at CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CC Neisseria proteins given in AABS8550 to AAF82554 to AAF21588 encode the CC Neisseria proteins given in AABS8550 to AAF825593, and AAF21589 to CC Neisseria invention. The NMB genome and fragments from it have CC Neisserial activity, and can be used in vaccines and gene therapy. CC Neisserial activity, and can be used in vaccines and gene therapy. CC Neisserial bacteria or as a diagnostic reagent for detection the proteins can be used in compositions for treating or preventing infection CC presence of Neisserial bacteria or of antibodies which binds to the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria or as a diagnostic reagent for detecting the Dateria. Computers, computer memory, computer seding frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide concert ferferity of in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1999;
08-OCT-1999;
28-FEB-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7696 GACGACCTGCTCGGCGTGATTTTTTCGAGGTTTTGTATCGGAAAATAAACGGATCGAAAG 7637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7636 CATCGTGGTGGTGT 7623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis B nucleotide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF21612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-647603/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000; 2000WO-US05928.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frames are used to detect, treat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis B full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                     more effective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggtcggggtctttt 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hickey E, 1
C, Mora M,
M, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appendix A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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2000GB-0004695.
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                                                                                                         vaccines than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterson J, Tettelin H,
Ratti G, Scarselli M,
                                                                                                         outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome sequence and open reading prevent Neisserial infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:113
                                                                                                     enic proteins which are proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masignani V;
Rappuoli R;
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Query Match Best Local S Matches 45

Similarity

21.4%; 60.8%;

Score 27.6; Pred. No. 34;

DB

Length 349980; Indels

Mismatches

29; 21;

Conservative

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                       Baker KP,
Gerritsen
Smith V,
                                                                                                  18 - FEB - 2000

22 - FEB - 2000

24 - FEB - 2000

24 - FEB - 2000

01 - MAR - 2000

20 - MAR - 2000

21 - MAR - 2000

31 - MAR - 2000

17 - MAY - 2000

17 - MAY - 2000
                                                          (GETH )
                                                                                                                                                                                                                                                                                                                                                                                       breast; prostate; cervical; tun
cartilage; ear; proliferation;
adipocyte; A-peptide; factor VJ
                                                                                                                                                                                                                                                                                                                       01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS21265 standard; cDNA; 1356 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 ggtcggggtctttt 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
2001-408281/43
DB; AAU12193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catcgtggtggtgt 291413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretory
                                                                                                                                                                                                                                                    -1999;
                                                          GENENTECH
                       ME, God
Stewart
                                                                                                                                   2000WO-US00277
2000WO-US00376
2000WO-US03565
2000WO-US04341
2000WO-US04342
2000WO-US04414
2000WO-US04414
2000WO-US04914
2000WO-US05601
2000WO-US05601
                                                                                                          2000WO-US07532.
2000WO-US08439.
2000WO-US13705.
                                                                                                                                                                                                                                                                                                                      2000WO-US32678
                               Goddard
                                                                                                                                                                                                                         99WO-US31243
                                                                                                                                                                                                                                                                                                                                                                                                              and transmembrane; PRO; mammalian; cancer; lung;
                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                    cervical; tumour necrosis factor-alpha; TNF-alpha; rollieration; glucose; free fatty acid; skeletal muscle; ide; factor VIIA; gene therapy; ss.
                       A, Go
Tumas
                             Deforge L, Desnoyers L,
A, Godowski PJ, Gurney !
                    D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  for PRO4314
                      Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                      Filvaroff E,
                             Sherwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Вb

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of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                             PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in perioyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
           Sequence 1356 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 43; 813pp; English.
292 A; 355 C; 373 G; 336 T; 0 other;
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RESULT 12
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Best Local
   07-MAY-1998;
02-JUN-1998;
22-JUL-1998;
                                                               07-MAY-1999;
                                                                                                                                                                                                    haematopoiesis regulation; chemotactic; chemokinetic; ligand; anti-inflammatory;
                                                                                                                                                                                                                                           Human; secreted protein; nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; suppression;
                                                                                              11-NOV-1999
                                                                                                                           W09957132-A1
                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                          Human secreted protein clone lv2_47 nucleotide sequence SEQ ID NO:35
                                                                                                                                                                                     tumour inhibition; gene
                                                                                                                                                                                                                                                                                                                                                                                           AAZ33333 standard; cDNA; 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgctgggattcttcgttggattaatccctcacctcctgggcgatgtggttttcttgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cttcgagcattactgacgacaaagaccccgaccgagatggtcgggggtctttttgttgtggg 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                               (first entry)
98US-0084564.
98US-0087645.
98US-0093712.
                                                             99WO-US09970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.2%;
                                                                                                                                                                                    therapy;
                                                                                                                                                                                                                  haemostatic; thrombolytic;
                                                                                                                                                                                                       cadherin;
                                                                                                                                                                                                                                 tissue growth; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27.4; DI
Pred. No. 7.1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1356;
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                                                                                                                                                                                                                                 inhibin;
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RESULT 1
AAH16020
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10-AUG-1998;
11-AUG-1998;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity/inhibin activity, chemotactic/chemokinetic activity, activity/inhibin activity, cativity, receptor/ligand activity, anti-inflammatory activity, cativity, receptor/ligand activity, anti-inflammatory activity, cativity. The polynucleotides are also stated to be useful for gene therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and AAY52998 to AAY53060 represent human secreted proteins, given in the present inversely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding secreted human proteins, derived adult placenta, adult retina, fetal brain, fetal
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P-PSDB; AAY53015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 44; Page 395-396; 492pp; English
28-JUL-2000; 2000EP-0116126
                           07-FEB-2001
                                                                                                         Human; primer;
                                                                                                                                  Human cDNA sequence SEQ ID NO:14672.
                                                                                                                                                                26-JUN-2001
                                                                                                                                                                                           AAH16020;
                                                                                                                                                                                                                   AAH16020 standard; cDNA; 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1670 BP;
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55; Conserv
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98US-0095880.
98US-0096068.
99US-0096068.
                                                                                                         detection; diagnosis; antisense therapy; gene therapy;
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                                                                                                                                                                entry)
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Agostino MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 G; 389
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Matches Best Query Match

Local

Similarity 54.

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Mismatches

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1878; 0;

21.2%;

Score 27.4; Pred. No. 7

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Human; secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disordevelopmental abnormality; foetal deficiency; blood disorder; ly

tumour; neurodegenerative disorder; l deficiency; blood disorder; lympho

Human secreted protein cDNA fragment containing gene

(first entry)

AAX37414 standard;

cDNA;

1951

803

tgctgtgacgtgttgtccaaccgtattattccggactagtt 124

ggctgtaacctgctggcccacttcatcaatgcctacctggt

743 84

24

cttcgagcattactgacgacaaagaccccgaccgagatggtcgggggtcttttttgttgtg

ctgctgggattcttcgttggattaatccctcacctcctgggcgatgtggttttcttgtgg

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The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotide; or (b) a combination of an oligonucleotide comprising a sequence complementary strand of a polynucleotide which comprises a 5'-end cc onlyonucleotide which comprises a 1'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a coligonucleotide comprises a 1'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cf in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs seasily without any specialised methods. AAH33165 to AAH3628 and CAAH33633 to AAH18742 represent human cold sequences; and AAH33629 to AAH3632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8;
Sequence 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs -
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Sugiyama T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
BP;
356
A; 526
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567
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A, Nagai K,
<u>ი</u>
429 T;
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  0 other;
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Matches
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Best Local :
                                                                                                                                                                                             the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood discretes, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine invention are represented in AAY07744-Y07850 and the encoding nucleic
                                                                                                                                                                                                                                                                                                                                                           This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brewer LA, L
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                            718
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1a;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
                   84
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tgctgtgacgtgttgtccaaccgtattattccggactagtt 124
                                                    cttcgagcattactgacgacaaagaccccgaccgagatggtcgggggtctttttgttgtgg
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970S-0056555.
970S-0056556:
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97US-0056726
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54.5%;
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e KA, Komatsoulis
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                                                                                                                                                             536 C; 576 G; 431 T;
                                                                                           Score 27.4; E
Pred. No. 7.9;
0; Mismatches
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Shi Y, Soppet DR;
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                                                                                                                    Length 1951;
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Sequence 2628 BP; 646 A;

662 C;

756 G;

564 T;

0 other

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Crelated microorganisms e.g. algae, archaed, bacteria, fungi and cetection and identification of an algal, archaed, bacteria, fungi and cetection and identification of an algal, archaed, bacterial, fungil and cetection and identification of an algal, archaed, bacterial, fungal contained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cetection of any bacterium, fungus or parasite in a sample and for the cetection of at least one antimicrobial agent resistance gene or at cetection of at least one antimicrobial agent resistance gene or at cetection and for identification of Streptococcus pneumoniae. Cetection and for identification of Streptococcus pneumoniae. Cetection cetection and for identification of Streptococcus pneumoniae. Cetection cetection and for identification of Streptococcus pneumoniae. Cetection cetection cetection cetection of a therapeutic agent which is effective against cetection cetectio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or primers and parasition acids of determined algal, archaeal, bacterial, fungal and parasitis species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting and used for producing probes and/or primers for detecting and used for producing probes and/or primers for detecting and used for producing probes and/or primers for detecting and used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and producing probes and producing problem and producing producing problem and producing problem and producing pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 1109-1110; 1580pp; English
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19-MAY-2000;
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Copyright (c) 1993 - 2000 Compugen Ltd
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359
FILING DATE: FEBTUARY 16, 1996
CLASSIFICATION APALICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION DATA:
APPLICATION NUMBER:

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TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FISH & RICHARDSON P. STREET: 4225 EXECUTIVE SQUARE, CITY: LA JOLLA STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WARREN, Patrick V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISH & RICHARDSON P.C.
25 EXECUTIVE SQUARE, STE 1400
                                      GENOMIC DNA
                                                                                                                       SINGLE
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TY 16, 1996
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US-08-672-850-11/c
; Sequence 11, Application US/08672850
; Patent No. 6140117
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                                                RESULT
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Best Local Similarity
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                                                                                                                                                                                                                    Matches
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Best Local
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TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
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APPLICANT: Araki, Toshiyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NINJURIN
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 907 base pairs
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                     434 CCCGAAGGCTGTAATGAAAACATTGATGACCACAGTGAAGAAGAACCAAGATGGTGGCTGC 375
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                                                                                              374 GITGITGAGCTGGTTGAGT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/672,850 FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
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                                                                                                                                                                                                                  Local Similarity
nes 46; Conserv
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                                                                                                              71 ctttttgttgtggtgctgt 89
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                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                          unknown
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; MOLECULE TYPE: US-08-672-850-11
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Best Local Similarity
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPETWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,850

FILING DATE: 24-UUL-1996

CIASCATTACATTON. 425
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ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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                                                                                                                                TITLE OF INVENTION: 34

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

ADDRESSEE: Flehr, Hohbach, Test, Suite 3400
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LENGTH: 907 base pairs
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TELECOMMUNICATION INFORMATION:
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                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 CCCGAAGGCTGTAATGAAAACATTGATGACCACAGTGAAGAAGACCAAGATGGTGGCTGC 375
                                                                                                                                                                                                                                                                                                                                                                                                       374 GTTGTTGAGCTGGTTGAGT 356
                                                                                                                           STREET: Four Embeddings CITY: San Francisco
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                    ZIP: .9411:
                                                                                                                         STATE:
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VENTION: NINJURIN
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Pred. No. 2.2;
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Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 907;
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CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 24-JUI

SEQUENCE CHARACTERISTICS:

ENGTH:

STRANDEDNESS: TOPOLOGY:

unknown

unknown

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Sequence 1, Application US/08804227C Patent No. 5876991
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                                                                                    TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    ATTORMEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-6
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TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                    TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 GTTGTTGAGCTGGTTGAGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICANT: Sutton, Kimberly L.
POLYKETIDE SYNTHASE GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruhstoss, Stuart A. Rosteck, Paul R., Jr.
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                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM Compatible
                                                                                                                                                                                                                   February 21, 1997
N: 435
           DNA (genomic)
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Mismatches
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US-08-674-887A-5/c
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; LOCATION: (87)..(1019)
US-09-198-092-1
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US-08-804-227C-1
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 1158
                                                                                                                                                                                                      Query Match
Best Local 9
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Best Local Similarity 55.6%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Omura, Mitsuo
APPLICANT: Ikoma, Yoshinori
APPLICANT: Komatsu, Akira
TITLE OF INVENTION: BETA-CAROTENE HYDROXYLASE GENE
FILE REFERENCE: 07898/033001
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/198,092A CURRENT FILING DATE: 1998-11-23 EARLIER APPLICATION NUMBER: JP97/331936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09198092A
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1997-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13202 CGCCTTCGGCCGCATGACGGTACCGATCCG 13173
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Citrus unshiu
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yano, Masamitsu
                                                                                                                  111 TGGCGGCCAATAGTCCGACCGCCATGGTGGGGTTTTGTTTTGTTTTACGAGGTTTTGGGTTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                               51
                                                                                            97 t 97
                                                                                                                                    37 tgacgacaaagaccccgaccgagatggtcgggggtctttttgttgtggtgctgtgacgtgt 96
                                                                                                                                                                                   Local Similarity 63.9 hes 39; Conservative
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NAME/KEY:
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31232..36067
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816..14234
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14351..19945
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                                                                                                                                                                                Score 25.8; DE Pred. No. 3.3; 0; Mismatches
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Conservative

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US-08-804-227C-1/c

GENERAL INFORMATION:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: Februa CLASSIFICATION: 435

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COLECULE TYPE:

TOPOLOGY:

STRANDEDNESS:

LENGTH:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy

COUNTRY:

USA

INDIANAPOLIS

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46285

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE:

Sequence 5,

, Application US/08674887A 5939300

tent No.

INFORMATION:

Robertson, Dan E.

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                                                                                                                                                      US-08-951-844-5/c
                                                                                                                     Sequence 5, Application US/08951844 Patent No. 6074860
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                         GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 09 TELECOMMUNICATION INFORMATION: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 03-JUL-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                               CORRESPONDENCE ADDRESS:
                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 856 TTTCGTCGT 848
                                                                                                                                                                                                                                                                           916 CATTGCCATTACCGTGACAATTACCGACGGTGTGGCCGCCAGCTGTGAGGGCTGCGGTTT 85
                                                                                            PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 92037
STREET:
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               ADDRESSEE:
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Adhikari, Robert S
WENTION: CATALASES
   6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                          Coding Sequence 1...2259
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FastSEQ for Windows Version 2.0
                                                                                           Robertson et al.
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                  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
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Pred. No. 4.
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/674,887
FILING DATE: July 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Charles J. Herron
NAME: Charles J. Herron
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: U5.708/461,244 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         916 CATTGCCATTACCGTGACAATTACCGACGGTGTGGCCGCCAGCTGTGAGGGCTGCGGTTT 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      856 TTTCGTCGT 848
                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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SOFTWARE: WORD PERFECT 5.1
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ZIP: 07068
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TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                     COUNTRY: UZIP: 07068
                                                                                                                                                                                                       CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                        STREET:
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                CLASSIFICATION:
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                                                                                                                                                                                                                                                          CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI STUART & OLSTEIN
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Pred. No. 4.4;
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REGISTRATION NUMBER

Ferraro, Gregory

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US-08-461-244-1
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Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-247-901C-1
                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-881-4766
NFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
DESCRIPTION: HYPOTHETICAL:
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 50341
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/057,531
FILING DATE: April 29, 1993
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                  STRANDEDNESS:
                                                                                                                                                                                                                       NAME: Bogosian, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/273
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/247,901C FILING DATE: May 23, 1994 CLASSIFICATION: 435
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                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                      nucleic acid
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                                                      linear
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                L5 shuttle phasmid sequence
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Pred. No. 5.3;
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CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,901
FILING DATE: May 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BOGOSTAIN, Elizabeth A
NAME: BOGOSTAIN, 20 011
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09075904 Patent No. 5994137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION:
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch 1.44 Mb storage diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1876 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGACGTATTCCCCGGGCCGT 1929
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE: POSITION IN GENOME:
                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                     ZIP: 10016
                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE:
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                                                                                                                                                                                                                                                                                                  90 Park Avenue
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                                                                                                      May 11,
                                                                                                                                                                                                                                                                                                                                                                            et al.
                                                                                                                                                                                                                                                                                                                                                             L5 SHUTTLE PHASMIDS
                                                         08/247,901
                                                                                                         US/09/075,904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.2;
Pred. No. 26;
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REFERENCE/DOCKET NUMBER: 96700/475

TELEX: TWX 710-581-47 NFORMATION FOR SEQ ID NO:

TELEFAX:

(212) 286-0854 or 286-0082 PWX 710-581-4766

TELEPHONE:

TELECOMMUNICATION INFORMATION:

(212)

697-5995

SEQUENCE CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                     Sequence 1, Application US/09426436
                                                                                                                                                                           ENERAL INFORMATION:
                                                                                                                                                                                                                                                                             1876 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGACGTATTCCCCGGCCGT 1929
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ORIGINAL SOURCE:
ORGANISM: L5 mycobacteriophage
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
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                                                                     CORRESPONDENCE ADDRESS
                                                                                                                            PPLICANT:
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CELL LINE:
ORGANELLE:
                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                              54 accgagatggtcggggtctttttgttgtggtgctgtggacgtgttgtccaaccgt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION:
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TISSUE TYPE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                    MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
COUNTRY:
                                         STREET:
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                                                       DDRESSEE
                                                                                                                                                                                        No. 6225066
             New York
                                         90 Park Avenue
                                                                                                                                             Barry R. Bloom
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                             William R. Jacobs, Jr.
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                                                                                                  REPORTER MYCOBACTERIOPHAGES
                                                                                                                MYCOBACTERIAL SPECIES-SPECIFIC
                                                                                                                              Hatfull
                                                       Rothstein & Ebenstein
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; Pred. No. 26;
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1773 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGACGTATTCCCCGGCCGT 1826

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US-09-426-436-1
                                             Matches
                                                         Query Match
Best Local Similarity
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TELEZ: TWX 710-581-4766
ENFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch 1.44 mb storage diskette
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ANTI-SENSE: I
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                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE: mycobactor
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                        EATURE:
                                                                                                                                                                                                                                                                                                                                                                      OSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
54 accgagatggtcgggggtctttttgttgtggtgctgttgacgtgttgtccaaccgt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: not applicable TISSUE TYPE: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: not applicabl INDIVIDUAL ISOLATE: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: mycobacteriophage L5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/426,436
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide
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                                                                                                                                                     395-405
                                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                 A Phage System
                                                                                                                                                                                                                               DNA Sequence, Structure and Gene Expression of Mycobacteriophage
                                                                                                                                                                                                                                                              Hatfull and
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                                                                                                                                                                                  Molecular Microbiology
                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   not applicable not applicable
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                                                         19.5%;
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                                           Score 25.2; D
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      particles
                                                                         DB 4;
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                                                                           Length 52297;
                                              Indels
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US-08-705-557-1
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                 IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Hatfull and:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: TWX 710-581-4766
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Willia
                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: n
                                                                                                                         OSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION: phage genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/833,431
FILING DATE: February 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 mb storage diskette
COMPUTER: IBM PC Compatible
                                                                                                                                            MMEDIATE SOURCE:
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APPLICATION NUMBER: (FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORD PROCESSOR (ASCII) CURRENT APPLICATION DATA:
                                                                                                                                                                                       TISSUE TYPE: not applicable CELL Type
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotide
STRANDEDNESS: single
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                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                               ORGANISM:
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              Hatfull and Sarkis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                  linear
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Sequence, Structure and Gene
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Graham F. Hatfi
                                                                                                                                                                                 not applicable
                                                                                                                                                                       not applicable
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                                                                                                                                                       not applicable
                                                                                                                                                                                                                                                                                                                                          no
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                                                                                                                                                                                                not applicable
                                                                                                                                    mycobacteriophage L5 particles
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                                                                                                                       entire genome
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Db.
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                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                   HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                             FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1773 ACCGTGACCATCGGCGACTCGCTGATGTCGAGCTGGGACGTATTCCCCGGCCGT 1826
                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                 TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                     EATURE
                                                                                                                                                           TOPOLOGI.

*OLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scott, June R.
APPLICANT: Froehlich, Barbara
APPLICANT: Caron, Judy
 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                             TYPE: nucleic acid
                                          LOCATION:
                                                       NAME/KEY:
                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 338
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                LOCATION:
                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 accgagatggtcgggggtctttttgttgtggtgctgtgacgtgttgtccaaccgt 107
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                                                                                                                                                                                                                            5798 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression of Mycobacteriophage A Phage System for Mycobacterial
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499..1215
mat_peptide
553..1212
                                       sig_peptide
499..552
                                                                                                                     Escherichia coli
                                                                                                                                                                                       circular
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                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                    double
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                                                                                                                                                                                                                                                                                                             6-95
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Pred. No. 26;
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NAME/KEY: LOCATION:

CDS 1255..1767

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US-08-483-101-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                    Sequence 100, Application US/08173510B Patent No. 5747296
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3190 CTTTTTATCGTAATGATAAAAGCGTTGATAATTGTAGTCACAATTACAGTGCGGGATGGA 3249
                                                                                                                                                                                                                                                                                                                                                                                    3310 C 3310
          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
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NAME/KEY:
                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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NAME/KEY:
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                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 cggggtctttttgttgtggtgctgtgacgtgttgtccaaccgtattattccggactagtt 124
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4505..5542
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1914..4433
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4451..4504
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4451..5545
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1836..1913
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1836..4436
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1324..1764
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1255..1323
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08/151,064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 2;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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                                                                                                           Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/991
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/88:
FILING DATE: 11-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION: (213) 489-1600
                                                                                                                                                                                                                                                TOPOLOGY: LINEAR MOLECULE TYPE: NUCLEIC
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
TELEX: 67-3510
                        63 gtcggggtcttttgttgtggtgctgtgacgtgttgtcca 102
                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 2...736
                                                                                                                                                                                                                                                                         STRANDEDNESS:
69 GTCCGCAGAATGAAGTAGAAATGGAGAAAGGTTTCGACGA 108
                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-NOVAPPLICATION NUMBER:
                                                                        ENGTH:
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1993
                                                                                                                                                                                                                                                                              SINGLE
                                                                                                                                19.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/060,433
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                                                                                                                                                                                                                                                                                                                                                                                                                         30,158
                                                                                                                                                                                                                                                                                                                                        100:
                                                                                                                 0;
                                                                                                                                Score 24.8; D
Pred. No. 6.6;
                                                                                                                    Mismatches
                                                                                                                                                DB 1; Length 799;
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Gaps

Search completed: March 28, \cdot 2002, 15:11:17 Job time: 7521 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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seq length:
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Gapop 10.0 , Gapext 1.0
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(c) 1993 - 2000 Compugen Ltd
            BG817831
AA517086
AJ282728
AV745983
BG817916
BG817916
BG817954
BG817854
BG817854
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BG817850
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                 AA517086
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BG817854
BG817854
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                                                                                                                        Description
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                                 1 ESSU0253
6 vh98f10.r
8 4A3A-ABB-
8 4A745983
1 ESSU0222
6 ESSU0338
6 ESSU0327
1 ESSU0276
1 ESSU0284
        ESSU0052
Drosophil
RC2-HT107
                                                                                                                                               JOURNAL
COMMENT
                                                  FEATURES
                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                              RESULT 1
BG817831/c
                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                 a a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    O
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Mattsson J.G.
Department of Parasitology (SWEPAR)
National Veterinary Institute
SE-751 89 Uppsala, Sweden
Tel: +46 18 674120
Fax: +46 18
                                                                                                                                                                                                                                                                                                                                                              228
228
288
288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jens.mattsson@sva.se
Similar to pir|T17405 scavenger recept or cysteine-rich protein
precursor - sea urchin (Strongyloce ntrotus purpuratus).
Seq primer: T3 primer
High quality sequence stop: 600.
Location/Qualifiers
                                                                                                                                                                                               Sarcoptes scabiei
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Acariformes; Sarcoptiformes; Astigmata; Sarcoptoidea; Sarcoptidae;
                                                                                                                                                                                                                                            BG817831 600 bp mRNA EST 22-MAY-2001
ESSU0253 S.scabiei cDNA library Sarcoptes scabiei cDNA clone
SAS0334 5', mRNA sequence.
BG817831 GI:14188811
                                                                                                                                                                  1 (bases 1 to 600)
Ljunggren,E.L., Nilsson,D., Nasl
Expressed sequence tag analysis
                                                                                                                                                                scabiei
                                                                                                                                                                                                                                  Sarcoptes scablei.
                                                                                                                                                                                                                                                                                                                                                                                               . 88 229
                                                                                                                                                                                                                                                                                                                                                            /organism="Sarcoptes scable1"
/db_xref="taxon:52283"
/clone="SAS0334"
/clone_lib="S.scabiei cDNA library"
                                                                                                                                                                                                                                                                                                                                                                            BF118685
BG247036
BF532038
BF781560
BF784104
BI248625
AA499104
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AL531914
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AA103400
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AI613789
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BE226847 us73d03.y
BE914799 60166782
BG965887 602829669
B1079667 602874603
BG922669 60282163
BG922669 602821635
BF384357 602046710
AU080797 AU080797
BF116685 601754973
BG247036 602359684
BF532038 602073004
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AI613789 vh98f10.y
BE945901 UI-M-BZ0-
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H76502 18207 Lambd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ggtcggggtctttttgttgttggtgctgtgacgtgttgtc 100
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57; Conser
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vh98f10.rl Barstead mouse myotubes MPLRB5
IMAGE:902347 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 524)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
Washb-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theising, B., Wylie, T., Lennon, G., Soares, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                    /organism="Mus musculus"
/strain="C3H"
                                                                                                                                                                                                      /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                            /clone="IMAGE:902347"
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57.6%;
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0; Mismatches
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                          ATCAATGCCTACTTGCTGCACG
  TGGGAGCAATTTAACGGCGCACTACTAACGGTAACGGACCAACACGTAATGTCCCGGGGT 125
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                                                                                                                  60;
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Meyerhofstrasse 1, 69117 Heidelberg,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Dimopoulos G Fotis C. Kafatos labor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae
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                                                                                                                                                                                                                                                                              /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806. The control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rapidly, forming contractile characteristic muscle protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="4A3A-ABB-D-05"
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hultz,J., Benes,V., Bork,P., Ansorge,W., Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
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Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 g
                                                                                                                                          Score 30.6;
Pred. No. 26;
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RESULT 5
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                                                                                                                                                                                            496 CCTCTGGGCACGTTTGTCTGTGTGCTGTAACCTGAAGTCAAACCTTAAGATAATGGA
                                                                                                                                                                                                                                                           436
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                                                                                           ESSU0222 S
SAS0293 5'
Sarcoptes scabiei
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
                     Sarcoptes scabiei.
Sarcoptes scabiei
                                                                                                                                                                                                                                                                                                                   63;
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Chinese M
351 Guo S
                                                                                                                          BG817800
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Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
                                                                  BG817800.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPA library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV/45983 NPA Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                Similarity 53.8
63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Z
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clone is available at Shanghai Hematology Institute
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Shoujing Road, Zhangjiang Hi-
Location/Qualifiers
                                                                                                          546 bp
S.scabiei c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NPAAZG08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pituitary"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                              note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone_lib="NPA"
                                                                                           mRNA sequence
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                                                                                                       cDNA library Sarcoptes scabiei cDNA clone
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Primates;
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Pred. No. 29;
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NPAAZG08
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Xu,Z., Zeng,L., Xu,S.,
Xu, Lu,G., Ye,M., Zhang,
                                                                                                                                                                                                                                                                                                                Indels
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                                                                            Unpublished (2001)
Contact: Mattsson J.G.
Contact: Mattsson J.G.
Department of Parasitology (SWEPAR)
National Veterinary Institute
SE-751 89 Uppsala, Sweden
Tel: +46 18 674120
Fax: +46 18
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BG817916.1
EST.
Email: jens.mattsson@sva.se
Similar to pir|T17405 scavenger recepto r cysteine-rich
precursor - sea urchin (Strongylocen trotus purpuratus)
Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG817916 577 bp mRNA ESSU0338 S.scablei cDNA library SAS0437 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Acariformes; Sarcoptiformes; Astigmata; Sarcoptoidea; Sarcoptidae;
                                                                                                                                                                                                                                    Expressed sequence
                                                                                                                                                                                                                                                      1 (bases 1 to 577)
Ljunggren, E.L., Nil
                                                                                                                                                                                                                                                                                             Sarcoptes.
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Tel: +46 18 674120
Fax: +46 18
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Ljunggren, E.L., Nil
Expressed sequence
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Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Parasitology (SWEPAR)
National Veterinary Institute
SE-751 89 Uppsala, Sweden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
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/clone_lib="95.scabiei cDNA library"
/clone_lib="95.scabiei mixed lifestage library wa
/note="The Sarcoptes scabiei mixed lifestage library wa
constructed by Jens G Mattsson. cDNAs were synthesized
from poly(A)+ RNA by oligo d(T) priming, size-selected
directionally cloned into the Uni-ZAP lambda vector
(Stratagene). The primary library was amplified on
XLI-Blue MRF cells."
136 c 121 g 133 t
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/db_xref="taxon:52283"
                                                                                                                                                                                                                                                                                                                                                                            scabiei.
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                                               Contact: Mattsson J.G.
Department of Parasitology (SWEPAR)
National Veterinary Institute
SE-751 89 Uppsala, Sweden
Tel: +46 18 674120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG817905 599 bp mRNA ESSU0327 S. scable1 cDNA library Sarcoptes SAS0423 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                Email: jens.mattsson@sva.se
Similar to pir|T17405 scavenger recepto r cysteine-rich protein
precursor - sea urchin (Strongylocen trotus purpuratus).
Seq.primer: T3 primer
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Sarcoptes scabiei
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ljunggren, E.L., Nilsson, D., Naslund, K. and Mattsson, J. Expressed sequence tag analysis of the parasitic mite
                                                                                                                                                                                                                                                                                                                                                             Fax: +46 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acariformes; Sarcoptiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG817905.1 GI:14188885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 599)
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                   166
                                                                                                                                                                                                                                            quality sequence stop: 599
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 577.
Location/Qualifiers
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                 D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="S.scablei cDNA library"
/note="The Sarcoptes scablei mixed lifestage library wa
constructed by Jens G Mattsson. cDNAs were synthesized
from poly(A)+ RNA by oligo d(T) priming, size-selected
directionally cloned into the Uni-ZAP lambda vector
(Stratagene). The primary library was amplified on
XLI_Blue MRF, cells."
a 143 c 129 g 145 t
                               /note-The Sarcoptes scablel mixed lifestage library was constructed by Jens G Mattsson. cDNAs were synthesized from poly(A)+ RNA by oligo d(T) priming, size-selected and directionally cloned into the Uni-ZAP lambda vector (Stratagene). The primary library was amplified on XLI-Blue MRF' cells.
                                                                                                                                                                     /organism="Sarcoptes scabiei"
/db_xref="taxon:52283"
/clone="SAS0423"
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/db_xref="taxon:52283"
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                   151 c
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Pred. No. 38;
0; Mismatches
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                 133 g
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Best Local S
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 347
                                                           407
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GTTTAGGGCATCTGTGGTGAGGTCTTTTGCAATGTCTTC
                                                         GACCATGAGGACGTGCACATGTTCTCGGGCATGAACGACCACAAGGAGCCCAATGAGAAT 348
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ESSU0276 S.scablei
SAS0362 5', mRNA se
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: jens.mattsson@sva.se
Similar to pirl[717405 scavenger recepto r cysteine-rich protein
precursor - sea urchin (Strongylocen trotus purpuratus).
Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SE-751 89 Uppsala,
Tel: +46 18 674120
Fax: +46 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Parasitology (S
National Veterinary Institute
SE-751 89 Uppsala, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mattsson J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scabiei
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
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EST.
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Ljunggren, E.L., Nil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acariformes;
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                                                                                                                                 Similarity
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                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop:
Location/Qualifiers
                                                                                                                     Conservative
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                                                                                                                                                                                                                         /clone_lib="S.scabie1 cDNA library"
/note="The Sarcoptes scabie1 mixed lifestage library was
constructed by Jens G Mattsson. CDNAs were synthesized
from poly(A)+ RNA by oligo d(T) priming, size-selected and
directionally cloned into the Uni-ZAP lambda vector
(Stratagene). The primary library was amplified on
XL1-Blue MRF', cells."
                                                                                                                                                                                                                                                                                                                                /clone="SAS0362"
                                                                                                                                                                                                                                                                                                                                              /organism="Sarcoptes scabiei"
/db_xref="taxon:52283"
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                                                                                                                                   23.48;
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i cDNA library
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                                                                                                                                 Score 30.2;
Pred. No. 39;
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analysis of the parasitic mite
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                                                                                                                     43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scabiei
                                                                                                                                                 Length
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                                                                                                                     Indels
                                                                                                                                                  657;
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cDNA clone
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Sarcoptes
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REFERENCE
AUTHORS
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BG817630/c
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AUTHORS
TITLE
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BG817862/c
                                                                                                         SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     62 ggtcggggtctttttgttgttgtggtgctgtgacgtgttgtc 100
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ESSU0052
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Sarcoptes.
1 (bases 1 to 720)
Ljunggren, E.L., Nilsson, D.,
                                                                                                                                                          SAS0067 5', mRNA sequence.
BG817630
                                                  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acariformes; Sarcoptiformes; Astigmata; Sarcoptoidea; S;
                                                                                          Sarcoptes scabiei
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High quality secure
                                                                                                         Sarcoptes scabiei.
                                                                                                                                           BG817630.1
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Tel: +46 18 674120
Fax: +46 18
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Department of Parasitology (SI
National Veterinary Institute
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Similar to pir[T17405 scavenger recepto r cysteine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 682)
Ljunggren, E.L., Nil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESSU0284 S.scabiei cDNA li
SAS0372 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                          720 bp mRNA ES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sarcoptes scabiei"
/db_xref="taxon:52283"
/clone="SAS0372"
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                                                                                                                                           GI:14188610
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Pred. No. 39;
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   Naslund, K.
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 and Mattsson, J.G
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                                                                                                                                                                                            scabiei cDNA clone
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                                                    Sarcoptidae;
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                                                                      Acari;
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RESULT 11
CNS017UC/c
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ORGANISM
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                      FEATURES
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                        Direct Submission
Submitted (23-UTL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                              Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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National Veterinary Institute
SE-751 89 Uppsala, Sweden
Tel: +46 18 674120
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Contact: Mattsson J.G.
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Similar to |pir|T17405 scavenger recep tor
                                                                                                                                                                                                                                                                                                                                                                                                                        fruit fly.
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Location/Qualifiers
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/db_xref="taxon:52283"
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                                                                                                                                                                                                                                                                                              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-HT1079
051200-015-e02&t3=2000-12-05&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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RC2-HT1079-051200-015-e02 HT
BF841751
                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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              /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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/db_xref="taxon:7227"
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                ttotgotogtagogattacttogagoattactgacgacaaagaccccgaccgagatggtc 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number Carti
                                                                                                                                                                                                                                                                                  This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weissenbach,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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                                                           Similarity 53.:
50; Conservative
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BI114606 1353 bp mRNA EST 26-JUN-2001 602861984F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5021228 5',
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Michigan State University
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,L., Ohlrogge,J., Raikhel,N., Somer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inote "Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated eticlated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA stages are staged to the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. "

99 c 119 g 118 t 19 others
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/strain="yar columbia"
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/clone="196N13T7"
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Somerville,S., Thomashow,M.,
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                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
  448
                                        123 ttcagcg 129
                                                                                 388 GTCCGGAAGTATATGCACTCGTGTGTGCTCATGCGAGCTAACCGTATACTAGGGCACACA 447
                                                                                                                                                                  328 ATCTGCCGCACGCGGCGAGTCGAGTGCGCCCAACCGCGAACAAAGAGACACGCCCCGAGACA 387
                                                                                                            63 gtcggggtctttttgttgtggtgctgtgacgtgttgtccaaccgtattattccggactag 122
                                                                                                                                                                                           CAGAGCG
                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1839 row: g column: 21
High quality sequence stop: 71.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1353)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
BI114606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI114606.1 GI:14565507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                        320 a
                                                                                                                                                                                                                                                   Conservative
    454
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="rhabdomyosarcoma"
/lab_host="pHIOB (phage=resistant)"
/note="organ: muscle; vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming using the placetionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGCAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 400 c 299 g 333 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5021228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="NIH_MGC_17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 1353
                                                                                                                                                                                                                                                                    22.8%;
                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                    Score 29.4;
Pred. No. 74;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                           1353;
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